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SEQUENCE LISTING

*Selby  
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<110> Genentech, Inc.  
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 35 40 45

Ala Lys Lys Asn Phe Gly Gly Asn Thr Ala Trp Glu Glu Lys Thr  
 50 55 60

Leu Ser Lys Tyr Glu Ser Ser Glu Ile Arg Leu Leu Glu Ile Leu Glu  
 65 70 75 80

Gly Leu Cys Glu Ser Ser Asp Phe Glu Cys Asn Gln Met Leu Glu Ala  
 85 90 95

Gln Glu Glu His Leu Glu Ala Trp Trp Leu Gln Leu Lys Ser Glu Tyr  
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Pro Asp Leu Phe Glu Trp Phe Cys Val Lys Thr Leu Lys Val Cys Cys  
 115 120 125

Ser Pro Gly Thr Tyr Gly Pro Asp Cys Leu Ala Cys Gln Gly Gly Ser  
 130 135 140

Gln Arg Pro Cys Ser Gly Asn Gly His Cys Ser Gly Asp Gly Ser Arg  
 145 150 155 160  
 Gln Gly Asp Gly Ser Cys Arg Cys His Met Gly Tyr Gln Gly Pro Leu  
 165 170 175  
 Cys Thr Asp Cys Met Asp Gly Tyr Phe Ser Ser Leu Arg Asn Glu Thr  
 180 185 190  
 His Ser Ile Cys Thr Ala Cys Asp Glu Ser Cys Lys Thr Cys Ser Gly  
 195 200 205  
 Leu Thr Asn Arg Asp Cys Gly Glu Cys Glu Val Gly Trp Val Leu Asp  
 210 215 220  
 Glu Gly Ala Cys Val Asp Val Asp Glu Cys Ala Ala Glu Pro Pro Pro  
 225 230 235 240  
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 Glu Glu Cys Asp Ser Ser Cys Val Gly Cys Thr Gly Glu Gly Pro Gly  
 260 265 270  
 Asn Cys Lys Glu Cys Ile Ser Gly Tyr Ala Arg Glu His Gly Gln Cys  
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 Ala Asp Val Asp Glu Cys Ser Leu Ala Glu Lys Thr Cys Val Arg Lys  
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 Asn Glu Asn Cys Tyr Asn Thr Pro Gly Ser Tyr Val Cys Val Cys Pro  
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Leu

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 aacagccctg gctgagggag ctgcagcgca gcagagtatc tgacggcgcc aggttgcgtta 180  
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                    30

      35
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Pro Phe Thr His Asp Phe Arg Lys Ala Gln Gln Arg Met Pro Ala Ile

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100		105	110
Ile Met Ala Asp Pro Thr Val Asn Val Pro Leu Leu Gly Thr Val Pro			
115		120	125
His Lys Ala Ser Val Val Gln Val Gly Phe Pro Cys Leu Gly Lys Gln			
130		135	140
Asp Gly Val Ala Ala Phe Glu Val Asp Val Ile Val Met Asn Ser Glu			
145		150	160
Gly Asn Thr Ile Leu Gln Thr Pro Gln Asn Ala Ile Phe Phe Lys Thr			
165		170	175
Cys Gln Gln Ala Glu Cys Pro Gly Gly Cys Arg Asn Gly Gly Phe Cys			
180		185	190
Asn Glu Arg Arg Ile Cys Glu Cys Pro Asp Gly Phe His Gly Pro His			
195		200	205
Cys Glu Lys Ala Leu Cys Thr Pro Arg Cys Met Asn Gly Gly Leu Cys			
210		215	220
Val Thr Pro Gly Phe Cys Ile Cys Pro Pro Gly Phe Tyr Gly Val Asn			
225		230	240
Cys Asp Lys Ala Asn Cys Ser Thr Thr Cys Phe Asn Gly Gly Thr Cys			
245		250	255
Phe Tyr Pro Gly Lys Cys Ile Cys Pro Pro Gly Leu Glu Gly Glu Gln			
260		265	270
Cys Glu Ile Ser Lys Cys Pro Gln Pro Cys Arg Asn Gly Gly Lys Cys			
275		280	285
Ile Gly Lys Ser Lys Cys Lys Cys Ser Lys Gly Tyr Gln Gly Asp Leu			
290		295	300
Cys Ser Lys Pro Val Cys Glu Pro Gly Cys Gly Ala His Gly Thr Cys			
305		310	320
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325		330	335
Cys Asn Lys Arg Tyr Glu Ala Ser Leu Ile His Ala Leu Arg Pro Ala			
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Gly Ala Gln Leu Arg Gln His Thr Pro Ser Leu Lys Lys Ala Glu Glu  
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<220>  
<223> Description of Artificial Sequence: Synthetic  
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<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

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oligonucleotide probe

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49

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<212> DNA  
<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

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<210> 10  
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<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

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<210> 11  
<211> 2197  
<212> DNA  
<213> Homo sapiens

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<212> PRT

<213> Homo sapiens

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35 40 45

Gln Glu Gln Asp Leu Cys Cys Arg Gly Arg Ala Asp Asp Cys Ala Leu  
50 55 60

Pro Tyr Leu Gly Ala Ile Cys Tyr Cys Asp Leu Phe Cys Asn Arg Thr  
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Val Ser Asp Cys Cys Pro Asp Phe Trp Asp Phe Cys Leu Gly Val Pro  
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Pro Pro Phe Pro Pro Ile Gln Gly Cys Met His Gly Gly Arg Ile Tyr  
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Pro Val Leu Gly Thr Tyr Trp Asp Asn Cys Asn Arg Cys Thr Cys Gln  
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His Arg Pro Gly

<210> 13  
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<223> a, t, c or g

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<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 14

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<210> 15  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

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22

<210> 16  
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<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

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50

<210> 17  
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<212> DNA  
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<210> 18  
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<212> PRT  
<213> Homo sapiens

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35 40 45

Pro Ala Ser Tyr Arg Leu Trp Gly Ala Pro Leu Gln Pro Thr Leu Gly  
50 55 60

Val Val Pro Gln Ala Ser Val Pro Leu Leu Thr Asp Leu Ala Gln Trp  
65 70 75 80

Glu Pro Val Leu Val Pro Glu Ala His Pro Asn Ala Ser Leu Thr Met  
85 90 95

Tyr Val Cys Thr Pro Val Pro His Pro Asp Pro Pro Met Ala Leu Ser  
100 105 110

Arg Thr Pro Thr Arg Gln Ile Ser Ser Ser Asp Thr Asp Pro Pro Ala  
115 120 125

Asp Gly Pro Ser Asn Pro Leu Cys Cys Cys Phe His Gly Pro Ala Phe  
130 135 140

Ser Thr Leu Asn Pro Val Leu Arg His Leu Phe Pro Gln Glu Ala Phe  
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Pro Ala His Pro Ile Tyr Asp Leu Ser Gln Val Trp Ser Val Val Ser  
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&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 19

tgctgtgcta ctcctgc当地 gccc

24

&lt;210&gt; 20

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<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 20

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24

<210> 21

<211> 44

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

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44

<210> 22

<211> 1200

<212> DNA

<213> Homo sapiens

<400> 22

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gcccttcccc aaccacgccc agaaggcagaa gcagttcgag ttgtgggtt ccgcacccac 600  
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tggcgggagg ggagccagat ccccgaggga ggaccctgag ggcgcgaag catccgagcc 780  
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gacgggtggc aggccttggc gaggaactga gtgtcaccct gatctcaggc caccagccctc 900  
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agacaaccgt ctggaggtgg ctgtcctcaa aatctgcttc tcggatctcc ctcatctgc 1020  
ccccagcccc caaactcctc ctggctagac tgttaggaagg gactttgtt tggctgggg 1080  
tttcaggaaa aaagaaaaggg agagagagga aaatagaggg ttgtccactc ctcacattcc 1140  
acgaccggc cctgcacccc acccccaact cccagccccg gaataaaaacc atttcctgc 1200

<210> 23

<211> 205

<212> PRT

<213> Homo sapiens

&lt;400&gt; 23

Met	Gly	Ala	Ala	Arg	Leu	Leu	Pro	Asn	Leu	Thr	Leu	Cys	Leu	Gln	Leu
1					5				10					15	

Leu	Ile	Leu	Cys	Cys	Gln	Thr	Gln	Tyr	Val	Arg	Asp	Gln	Gly	Ala	Met
					20			25				30			

Thr	Asp	Gln	Leu	Ser	Arg	Arg	Gln	Ile	Arg	Glu	Tyr	Gln	Leu	Tyr	Ser
					35			40				45			

Arg	Thr	Ser	Gly	Lys	His	Val	Gln	Val	Thr	Gly	Arg	Arg	Ile	Ser	Ala
					50			55			60				

Thr	Ala	Glu	Asp	Gly	Asn	Lys	Phe	Ala	Lys	Leu	Ile	Val	Glu	Thr	Asp
					65			70			75		80		

Thr	Phe	Gly	Ser	Arg	Val	Arg	Ile	Lys	Gly	Ala	Glu	Ser	Glu	Lys	Tyr
					85			90			95				

Ile	Cys	Met	Asn	Lys	Arg	Gly	Lys	Leu	Ile	Gly	Lys	Pro	Ser	Gly	Lys
					100			105			110				

Ser	Lys	Asp	Cys	Val	Phe	Thr	Glu	Ile	Val	Leu	Glu	Asn	Asn	Tyr	Thr
					115			120			125				

Ala	Phe	Gln	Asn	Ala	Arg	His	Glu	Gly	Trp	Phe	Met	Ala	Phe	Thr	Arg
					130			135			140				

Gln	Gly	Arg	Pro	Arg	Gln	Ala	Ser	Arg	Ser	Arg	Gln	Asn	Gln	Arg	Glu
					145			150			155		160		

Ala	His	Phe	Ile	Lys	Arg	Leu	Tyr	Gln	Gly	Gln	Leu	Pro	Phe	Pro	Asn
					165			170			175				

His	Ala	Glu	Lys	Gln	Lys	Gln	Phe	Glu	Phe	Val	Gly	Ser	Ala	Pro	Thr
					180			185			190				

Arg	Arg	Thr	Lys	Arg	Thr	Arg	Arg	Pro	Gln	Pro	Leu	Thr			
					195			200			205				

&lt;210&gt; 24

&lt;211&gt; 28

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 24

cagtacgtga gggaccaggg cgccatga

28

&lt;210&gt; 25

<211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 25  
 ccggtgacct gcacgtgctt gccca 24

<210> 26  
 <211> 41  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<220>  
 <221> modified\_base  
 <222> (21)  
 <223> a, t, c or g

<400> 26  
 gcggatctgc cgccctgctca nctggtcggt catggcgccc t 41

<210> 27  
 <211> 2479  
 <212> DNA  
 <213> Homo sapiens

<400> 27  
 acttgccatc acctgttgcc agtgtggaaa aattctccct gttgaatttt ttgcacatgg 60  
 aggacagcag caaagaggc aacacaggct gataagacca gagacagcag ggagattatt 120  
 ttaccatacg ccctcaggac gtccctcta gctggagtcc tggacttcaa cagaacccc 180  
 tccagtcatt ttgattttgc ttttttctt ttctttttcc caccacattt 240  
 tattttattt ccgtacttca gaaatgggcc tacagaccac aaagtggccc agccatgggg 300  
 ctttttcctt gaagtcttgg ctatcattt ccctggggct ctactcacag gtgtccaaac 360  
 tcctggcctg cccttagtgtg tgccgctgac agaggaactt tggactactgt aatgagcgaa 420  
 gcttgacctc agtgccttgg gggatcccg aggccgtaac cgtactctac ctccacaaca 480  
 accaaattaa taatgctgga tttcctgcag aactgcacaa tgtacagtgc gtgcacacgg 540  
 tctacctgta tggcaaccaa ctggacgaat tccccatgaa cttcccaag aatgtcagag 600  
 ttctccattt gcaggaaaac aatattcaga ccatttcacg ggctgctttt gcccagctct 660  
 tgaagcttga agagctgcac ctggatgaca actccatatac cacagtgggg gtgaaagacg 720  
 gggcccttccg ggaggctatt agcctcaaattt tggacttgc tggacttgc aatgtcagag 780  
 gtgtgcctgt tggacttgc aagagctgag agtggatgaa aatgtcagag 840  
 ctgtcatatc cgacatggcc ttccagaatc tcacgagctt ggacgtctt attgtggacg 900  
 ggaacctcctt gaccaacaag ggtatcgccg agggcacctt cagccatctc accaagctca 960  
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 atctgatcag gctctatttgc caggacaacc agataaaacca cattcctttg acagccttct 1080  
 caaatctgctgca taagctggaa cggctggata tatccaacaa ccaactgcgg atgctgactc 1140

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cgtcccacag	catgggctcc	ccctttctgc	tggcgggctt	gatcgggggc	gcggtgatata	1920
tttgtgctggt	ggttttgctc	agcgttttt	gctggcatat	gcacaaaaag	ggcgctaca	1980
cctcccaagaa	gtggaaatac	aaccggggcc	ggcggaaaga	tgattattgc	gaggcaggca	2040
ccaagaagga	caactccatc	ctggagatga	cagaaaccag	ttttcagatc	gtctcccaa	2100
ataacgatca	actccttaaa	ggagattca	gactgcagcc	catttacacc	ccaaatgggg	2160
gcattaatta	cacagactgc	catatcccc	acaacatgcg	atactgcaac	agcagcgtc	2220
cagacctgga	gcactgccat	acgtgacagc	cagaggccca	gcgttatcaa	ggcggacaat	2280
tagactcttgc	agaacacact	cgtgtgtca	cataaagaca	cgcagattac	atttgataaa	2340
tgttacacag	atgcatttgc	gcatttgaat	actctgtaa	ttatacggtg	tactatataa	2400
tgggatttaa	aaaaagtgc	atctttcta	tttcaagtt	attacaaaca	gttttgcata	2460
tctttgtttt	ttaaatctt					2479

<210> 28

<211> 660

<212> PRT

<213> Homo sapiens

<400> 28

Met	Gly	Leu	Gln	Thr	Thr	Lys	Trp	Pro	Ser	His	Gly	Ala	Phe	Phe	Leu
1					5					10					15

Lys Ser Trp Leu Ile Ile Ser Leu Gly Leu Tyr Ser Gln Val Ser Lys  
20 25 30

Leu Leu Ala Cys Pro Ser Val Cys Arg Cys Asp Arg Asn Phe Val Tyr  
35 40 45

Cys Asn Glu Arg Ser Leu Thr Ser Val Pro Leu Gly Ile Pro Glu Gly  
50 55 60

Val	Thr	Val	Leu	Tyr	Leu	His	Asn	Asn	Gln	Ile	Asn	Asn	Ala	Gly	Phe
65				70						75					80

Pro Ala Glu Leu His Asn Val Gln Ser Val His Thr Val Tyr Leu Tyr  
85 90 95

Gly Asn Gln Leu Asp Glu Phe Pro Met Asn Leu Pro Lys Asn Val Arg  
100 105 110

Val Leu His Leu Gln Glu Asn Asn Ile Gln Thr Ile Ser Arg Ala Ala  
115 120 125

Leu Ala Gln Leu Leu Lys Leu Glu Glu Leu His Leu Asp Asp Asn Ser  
 130 135 140  
 Ile Ser Thr Val Gly Val Glu Asp Gly Ala Phe Arg Glu Ala Ile Ser  
 145 150 155 160  
 Leu Lys Leu Leu Phe Leu Ser Lys Asn His Leu Ser Ser Val Pro Val  
 165 170 175  
 Gly Leu Pro Val Asp Leu Gln Glu Leu Arg Val Asp Glu Asn Arg Ile  
 180 185 190  
 Ala Val Ile Ser Asp Met Ala Phe Gln Asn Leu Thr Ser Leu Glu Arg  
 195 200 205  
 Leu Ile Val Asp Gly Asn Leu Leu Thr Asn Lys Gly Ile Ala Glu Gly  
 210 215 220  
 Thr Phe Ser His Leu Thr Lys Leu Lys Glu Phe Ser Ile Val Arg Asn  
 225 230 235 240  
 Ser Leu Ser His Pro Pro Pro Asp Leu Pro Gly Thr His Leu Ile Arg  
 245 250 255  
 Leu Tyr Leu Gln Asp Asn Gln Ile Asn His Ile Pro Leu Thr Ala Phe  
 260 265 270  
 Ser Asn Leu Arg Lys Leu Glu Arg Leu Asp Ile Ser Asn Asn Gln Leu  
 275 280 285  
 Arg Met Leu Thr Gln Gly Val Phe Asp Asn Leu Ser Asn Leu Lys Gln  
 290 295 300  
 Leu Thr Ala Arg Asn Asn Pro Trp Phe Cys Asp Cys Ser Ile Lys Trp  
 305 310 315 320  
 Val Thr Glu Trp Leu Lys Tyr Ile Pro Ser Ser Leu Asn Val Arg Gly  
 325 330 335  
 Phe Met Cys Gln Gly Pro Glu Gln Val Arg Gly Met Ala Val Arg Glu  
 340 345 350  
 Leu Asn Met Asn Leu Leu Ser Cys Pro Thr Thr Pro Gly Leu Pro  
 355 360 365  
 Leu Phe Thr Pro Ala Pro Ser Thr Ala Ser Pro Thr Thr Gln Pro Pro  
 370 375 380  
 Thr Leu Ser Ile Pro Asn Pro Ser Arg Ser Tyr Thr Pro Pro Thr Pro  
 385 390 395 400  
 Thr Thr Ser Lys Leu Pro Thr Ile Pro Asp Trp Asp Gly Arg Glu Arg

405	410	415
Val Thr Pro Pro Ile Ser Glu Arg Ile Gln Leu Ser Ile His Phe Val		
420	425	430
Asn Asp Thr Ser Ile Gln Val Ser Trp Leu Ser Leu Phe Thr Val Met		
435	440	445
Ala Tyr Lys Leu Thr Trp Val Lys Met Gly His Ser Leu Val Gly Gly		
450	455	460
Ile Val Gln Glu Arg Ile Val Ser Gly Glu Lys Gln His Leu Ser Leu		
465	470	475
Val Asn Leu Glu Pro Arg Ser Thr Tyr Arg Ile Cys Leu Val Pro Leu		
485	490	495
Asp Ala Phe Asn Tyr Arg Ala Val Glu Asp Thr Ile Cys Ser Glu Ala		
500	505	510
Thr Thr His Ala Ser Tyr Leu Asn Asn Gly Ser Asn Thr Ala Ser Ser		
515	520	525
His Glu Gln Thr Thr Ser His Ser Met Gly Ser Pro Phe Leu Leu Ala		
530	535	540
Gly Leu Ile Gly Gly Ala Val Ile Phe Val Leu Val Val Leu Leu Ser		
545	550	555
Val Phe Cys Trp His Met His Lys Lys Gly Arg Tyr Thr Ser Gln Lys		
565	570	575
Trp Lys Tyr Asn Arg Gly Arg Arg Lys Asp Asp Tyr Cys Glu Ala Gly		
580	585	590
Thr Lys Lys Asp Asn Ser Ile Leu Glu Met Thr Glu Thr Ser Phe Gln		
595	600	605
Ile Val Ser Leu Asn Asn Asp Gln Leu Leu Lys Gly Asp Phe Arg Leu		
610	615	620
Gln Pro Ile Tyr Thr Pro Asn Gly Gly Ile Asn Tyr Thr Asp Cys His		
625	630	635
Ile Pro Asn Asn Met Arg Tyr Cys Asn Ser Ser Val Pro Asp Leu Glu		
645	650	655
His Cys His Thr		
660		
<210> 29		
<211> 21		
<212> DNA		

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 29

cggcttaccc gttatggcaac c

21

<210> 30

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 30

gcaggacaac cagataaacc ac

22

<210> 31

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 31

acgcagattt gagaaggctg tc

22

<210> 32

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 32

ttcacgggct gctcttgccc agctcttgaa gcttgaagag ctgcac

46

<210> 33

<211> 3449

<212> DNA

<213> Homo sapiens

<400> 33

acttggagca agcggcgccg gcggagacag aggcagaggc agaagctggg gctccgtcct 60  
cgccctccac gagcgtatccc cgaggagagc cgccggccctc ggcgaggcga agaggccgac 120



ctgtagaaca ctggccatag gaaatgctgt tttttgtac tggactttac cttgatata 3360  
 gtatatggat gtatgcataa aatcatagga catatgtact tgtggAACAA gttggatttt 3420  
 ttatacaata ttAAAATTCA ccacttcag 3449

<210> 34  
 <211> 915  
 <212> PRT  
 <213> Homo sapiens

<400> 34  
 Met Glu Lys Met Leu Ala Gly Cys Phe Leu Leu Ile Leu Gly Gln Ile  
 1 5 10 15  
 Val Leu Leu Pro Ala Glu Ala Arg Glu Arg Ser Arg Gly Arg Ser Ile  
 20 25 30  
 Ser Arg Gly Arg His Ala Arg Thr His Pro Gln Thr Ala Leu Leu Glu  
 35 40 45  
 Ser Ser Cys Glu Asn Lys Arg Ala Asp Leu Val Phe Ile Ile Asp Ser  
 50 55 60  
 Ser Arg Ser Val Asn Thr His Asp Tyr Ala Lys Val Lys Glu Phe Ile  
 65 70 75 80  
 Val Asp Ile Leu Gln Phe Leu Asp Ile Gly Pro Asp Val Thr Arg Val  
 85 90 95  
 Gly Leu Leu Gln Tyr Gly Ser Thr Val Lys Asn Glu Phe Ser Leu Lys  
 100 105 110  
 Thr Phe Lys Arg Lys Ser Glu Val Glu Arg Ala Val Lys Arg Met Arg  
 115 120 125  
 His Leu Ser Thr Gly Thr Met Thr Gly Leu Ala Ile Gln Tyr Ala Leu  
 130 135 140  
 Asn Ile Ala Phe Ser Glu Ala Glu Gly Ala Arg Pro Leu Arg Glu Asn  
 145 150 155 160  
 Val Pro Arg Val Ile Met Ile Val Thr Asp Gly Arg Pro Gln Asp Ser  
 165 170 175  
 Val Ala Glu Val Ala Ala Lys Ala Arg Asp Thr Gly Ile Leu Ile Phe  
 180 185 190  
 Ala Ile Gly Val Gly Gln Val Asp Phe Asn Thr Leu Lys Ser Ile Gly  
 195 200 205  
 Ser Glu Pro His Glu Asp His Val Phe Leu Val Ala Asn Phe Ser Gln  
 210 215 220  
 Ile Glu Thr Leu Thr Ser Val Phe Gln Lys Lys Leu Cys Thr Ala His

225	230	235	240
Met Cys Ser Thr Leu Glu His Asn Cys Ala His Phe Cys Ile Asn Ile			
245		250	255
Pro Gly Ser Tyr Val Cys Arg Cys Lys Gln Gly Tyr Ile Leu Asn Ser			
260	265		270
Asp Gln Thr Thr Cys Arg Ile Gln Asp Leu Cys Ala Met Glu Asp His			
275	280		285
Asn Cys Glu Gln Leu Cys Val Asn Val Pro Gly Ser Phe Val Cys Gln			
290	295	300	
Cys Tyr Ser Gly Tyr Ala Leu Ala Glu Asp Gly Lys Arg Cys Val Ala			
305	310	315	320
Val Asp Tyr Cys Ala Ser Glu Asn His Gly Cys Glu His Glu Cys Val			
325	330		335
Asn Ala Asp Gly Ser Tyr Leu Cys Gln Cys His Glu Gly Phe Ala Leu			
340	345		350
Asn Pro Asp Glu Lys Thr Cys Thr Arg Ile Asn Tyr Cys Ala Leu Asn			
355	360		365
Lys Pro Gly Cys Glu His Glu Cys Val Asn Met Glu Glu Ser Tyr Tyr			
370	375	380	
Cys Arg Cys His Arg Gly Tyr Thr Leu Asp Pro Asn Gly Lys Thr Cys			
385	390	395	400
Ser Arg Val Asp His Cys Ala Gln Gln Asp His Gly Cys Glu Gln Leu			
405	410		415
Cys Leu Asn Thr Glu Asp Ser Phe Val Cys Gln Cys Ser Glu Gly Phe			
420	425		430
Leu Ile Asn Glu Asp Leu Lys Thr Cys Ser Arg Val Asp Tyr Cys Leu			
435	440		445
Leu Ser Asp His Gly Cys Glu Tyr Ser Cys Val Asn Met Asp Arg Ser			
450	455	460	
Phe Ala Cys Gln Cys Pro Glu Gly His Val Leu Arg Ser Asp Gly Lys			
465	470	475	480
Thr Cys Ala Lys Leu Asp Ser Cys Ala Leu Gly Asp His Gly Cys Glu			
485	490		495
His Ser Cys Val Ser Ser Glu Asp Ser Phe Val Cys Gln Cys Phe Glu			
500	505		510

Gly Tyr Ile Leu Arg Glu Asp Gly Lys Thr Cys Arg Arg Lys Asp Val  
 515 520 525  
 Cys Gln Ala Ile Asp His Gly Cys Glu His Ile Cys Val Asn Ser Asp  
 530 535 540  
 Asp Ser Tyr Thr Cys Glu Cys Leu Glu Gly Phe Arg Leu Ala Glu Asp  
 545 550 555 560  
 Gly Lys Arg Cys Arg Arg Lys Asp Val Cys Lys Ser Thr His His Gly  
 565 570 575  
 Cys Glu His Ile Cys Val Asn Asn Gly Asn Ser Tyr Ile Cys Lys Cys  
 580 585 590  
 Ser Glu Gly Phe Val Leu Ala Glu Asp Gly Arg Arg Cys Lys Lys Cys  
 595 600 605  
 Thr Glu Gly Pro Ile Asp Leu Val Phe Val Ile Asp Gly Ser Lys Ser  
 610 615 620  
 Leu Gly Glu Glu Asn Phe Glu Val Val Lys Gln Phe Val Thr Gly Ile  
 625 630 635 640  
 Ile Asp Ser Leu Thr Ile Ser Pro Lys Ala Ala Arg Val Gly Leu Leu  
 645 650 655  
 Gln Tyr Ser Thr Gln Val His Thr Glu Phe Thr Leu Arg Asn Phe Asn  
 660 665 670  
 Ser Ala Lys Asp Met Lys Lys Ala Val Ala His Met Lys Tyr Met Gly  
 675 680 685  
 Lys Gly Ser Met Thr Gly Leu Ala Leu Lys His Met Phe Glu Arg Ser  
 690 695 700  
 Phe Thr Gln Gly Glu Gly Ala Arg Pro Leu Ser Thr Arg Val Pro Arg  
 705 710 715 720  
 Ala Ala Ile Val Phe Thr Asp Gly Arg Ala Gln Asp Asp Val Ser Glu  
 725 730 735  
 Trp Ala Ser Lys Ala Lys Ala Asn Gly Ile Thr Met Tyr Ala Val Gly  
 740 745 750  
 Val Gly Lys Ala Ile Glu Glu Glu Leu Gln Glu Ile Ala Ser Glu Pro  
 755 760 765  
 Thr Asn Lys His Leu Phe Tyr Ala Glu Asp Phe Ser Thr Met Asp Glu  
 770 775 780  
 Ile Ser Glu Lys Leu Lys Lys Gly Ile Cys Glu Ala Leu Glu Asp Ser  
 785 790 795 800

Asp Gly Arg Gln Asp Ser Pro Ala Gly Glu Leu Pro Lys Thr Val Gln  
 805 810 815  
 Gln Pro Thr Glu Ser Glu Pro Val Thr Ile Asn Ile Gln Asp Leu Leu  
 820 825 830  
 Ser Cys Ser Asn Phe Ala Val Gln His Arg Tyr Leu Phe Glu Glu Asp  
 835 840 845  
 Asn Leu Leu Arg Ser Thr Gln Lys Leu Ser His Ser Thr Lys Pro Ser  
 850 855 860  
 Gly Ser Pro Leu Glu Glu Lys His Asp Gln Cys Lys Cys Glu Asn Leu  
 865 870 875 880  
 Ile Met Phe Gln Asn Leu Ala Asn Glu Glu Val Arg Lys Leu Thr Gln  
 885 890 895  
 Arg Leu Glu Glu Met Thr Gln Arg Met Glu Ala Leu Glu Asn Arg Leu  
 900 905 910

Arg Tyr Arg  
915

<210> 35  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 35  
 gtgaccctgg ttgtgaatac tcc

23

<210> 36  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 36  
 acagccatgg tctatacgctt gg

22

<210> 37  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 37  
 gcctgtcagt gtcctgaggg acacgtgctc cgcagcgatg ggaag

45

<210> 38  
 <211> 1813  
 <212> DNA  
 <213> Homo sapiens

<400> 38  
 ggagccgccc tgggtgtca gggctcggt cccgcgcacg ctccggccgt cgcgcaaggct 60  
 cggcacctgc aggtccgtgc gtccccggc tggcgccccct gactccgtcc cggccaggga 120  
 gggccatgat ttccctcccg gggccccctgg tgaccaactt gctgcgggtt ttgttcctgg 180  
 ggctgagtgc cctcgcgccc ccctcgccgg cccagctgca actgcacttg cccgcacaacc 240  
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 aggtgtcttc atccccagcca tgggaggtgc cctttgtat gtggttcttc aaacagaaaag 360  
 aaaaggagga tcaggtgttg tcttacatca atggggtcac aacaagcaaa cctggagtat 420  
 ccttggctca ctccatggcc tcccggaacc tgcctcgat gctggagggt ctccaggaga 480  
 aagactctgg cccctacagc tgcctcgat atgtgcaaga caaacaaggc aaatctaggg 540  
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 ctggagtcta tgtctgcaag gcccacaatg aggtgggcac tgcccaatgt aatgtgacgc 840  
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 ccccccattttt tgggggggtt tcttcctctt gcttgcatttcc catgggtgtt gtgcctgtta 1260  
 tgggtgccttc ccagagtcaa gtcggcttc tggatgtatg accccaccac tcattggctt 1320  
 aaggattttgg ggtcttcctt tcctataagg gtcacctcta gcacagaggc ctgagtcatg 1380  
 gggaaagatgc acacttcgtt cccttagtac tctgccttttta ctgtggaaaa 1440  
 accatctcgtt taagacctaa gtgtccagga gacagaagga gaagagggaa tggatctgg 1500  
 attgggagga gcttcaccc accccctgact ctcctttagt aagccagctg ctgaaatttt 1560  
 ctactccatcca agagtggggggcagagactt ccagtcaactg agtctcccttgc gccccttgc 1620  
 tctgtacccccc accccatatctt aacaccaccc ttggctccca ctccagctcc ctgttattgtt 1680  
 ataaccttcgtt aggctggctt gtttaggttt tactggggca gaggataggaa aatctttat 1740  
 taaaactaac atgaaatatg tggatgttttcc atttgcataat ttaaataaag atacataatg 1800  
 tttgtatgaa aaa 1813

<210> 39  
 <211> 390  
 <212> PRT  
 <213> Homo sapiens

<400> 39  
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Leu His Leu Pro Ala Asn Arg Leu Gln Ala Val Glu Gly Gly Glu Val			
35	40	45	
Val Leu Pro Ala Trp Tyr Thr Leu His Gly Glu Val Ser Ser Ser Gln			
50	55	60	
Pro Trp Glu Val Pro Phe Val Met Trp Phe Phe Lys Gln Lys Glu Lys			
65	70	75	80
Glu Asp Gln Val Leu Ser Tyr Ile Asn Gly Val Thr Thr Ser Lys Pro			
85	90	95	
Gly Val Ser Leu Val Tyr Ser Met Pro Ser Arg Asn Leu Ser Leu Arg			
100	105	110	
Leu Glu Gly Leu Gln Glu Lys Asp Ser Gly Pro Tyr Ser Cys Ser Val			
115	120	125	
Asn Val Gln Asp Lys Gln Gly Lys Ser Arg Gly His Ser Ile Lys Thr			
130	135	140	
Leu Glu Leu Asn Val Leu Val Pro Pro Ala Pro Pro Ser Cys Arg Leu			
145	150	155	160
Gln Gly Val Pro His Val Gly Ala Asn Val Thr Leu Ser Cys Gln Ser			
165	170	175	
Pro Arg Ser Lys Pro Ala Val Gln Tyr Gln Trp Asp Arg Gln Leu Pro			
180	185	190	
Ser Phe Gln Thr Phe Phe Ala Pro Ala Leu Asp Val Ile Arg Gly Ser			
195	200	205	
Leu Ser Leu Thr Asn Leu Ser Ser Ser Met Ala Gly Val Tyr Val Cys			
210	215	220	
Lys Ala His Asn Glu Val Gly Thr Ala Gln Cys Asn Val Thr Leu Glu			
225	230	235	240
Val Ser Thr Gly Pro Gly Ala Ala Val Val Ala Gly Ala Val Val Gly			
245	250	255	
Thr Leu Val Gly Leu Gly Leu Leu Ala Gly Leu Val Leu Leu Tyr His			
260	265	270	
Arg Arg Gly Lys Ala Leu Glu Glu Pro Ala Asn Asp Ile Lys Glu Asp			
275	280	285	

Ala Ile Ala Pro Arg Thr Leu Pro Trp Pro Lys Ser Ser Asp Thr Ile  
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 Ser Lys Asn Gly Thr Leu Ser Ser Val Thr Ser Ala Arg Ala Leu Arg  
 305 310 315 320  
 Pro Pro His Gly Pro Pro Arg Pro Gly Ala Leu Thr Pro Thr Pro Ser  
 325 330 335  
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 340 345 350  
 Ala His Pro Gln Pro Ile Ser Pro Ile Pro Gly Gly Val Ser Ser Ser  
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 370 375 380

Gln Ala Gly Ser Leu Val  
385 390

<210> 40  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 40  
 aggtctcca ggagaaagac tc

22

<210> 41  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 41  
 atttgtggcc ttgcagacat agac

24

<210> 42  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 42  
ggccacagca tcaaaacctt agaactcaat gtactggttc ctccagctcc 50

<210> 43  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 43  
gtgtgacaca gcgtgggc 18

<210> 44  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 44  
gaccggcagg cttctgcg 18

<210> 45  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 45  
cagcagcttc agccaccagg agtgg 25

<210> 46  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 46  
ctgagccgtg ggctgcagtc tcgc 24

<210> 47

<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 47  
ccgactacga ctggttcttc atcatgcagg atgacacata tgtgc 45

<210> 48  
<211> 2822  
<212> DNA  
<213> Homo sapiens

<400> 48  
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gtgaaatacg caatggattt gaagcctgct attgcaacat gggattttca gaaaatgggt 180  
tcacaatttg tgaagatgtat aatgaatgtg gaaatttaac tcagtcctgt ggcgaaaatg 240  
ctaattgcac taacacagaa ggaagtttattt attgtatgtg tgtacctggc ttcatatcca 300  
gcagtaacca agacagggtt atcactaatg atggacccgt ctgtatagaa aatgtgaatg 360  
caaactgcca ttttagataat gtctgtatag ctgcaaatat taataaaact ttaacaaaaaa 420  
tcagatccat aaaagaacctt gtggctttgc tacaagaagt ctatagaaat tctgtgacag 480  
atcttcacc aacagatata attacatata tagaaatattt agctgaatca tcttcatttt 540  
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acctccacaa attgaaaaaaaaaaaaaaaaaaa aaaaaaaaaaaa aaaaaaaaaaaa 2820  
aa 2822

<210> 49

<211> 690

<212> PRT

<213> Homo sapiens

<400> 49

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                   20                  25                          30

Cys Glu Ile Arg Asn Gly Ile Glu Ala Cys Tyr Cys Asn Met Gly Phe  
                  35                 40                 45

Ser Gly Asn Gly Val Thr Ile Cys Glu Asp Asp Asn Glu Cys Gly Asn  
50 55 60

Leu Thr Gln Ser Cys Gly Glu Asn Ala Asn Cys Thr Asn Thr Glu Gly  
65 . . . 70 . . . 75 . . . 80

Ser Tyr Tyr Cys Met Cys Val Pro Gly Phe Arg Ser Ser Ser Asn Gln  
85 90 95

Asp Arg Phe Ile Thr Asn Asp Gly Thr Val Cys Ile Glu Asn Val Asn  
           100                 105                 110

Ala Asn Cys His Leu Asp Asn Val Cys Ile Ala Ala Asn Ile Asn Lys  
115 120 125

Thr Leu Thr Lys Ile Arg Ser Ile Lys Glu Pro Val Ala Leu Leu Gln  
130 135 140

Glu Val Tyr Arg Asn Ser Val Thr Asp Leu Ser Pro Thr Asp Ile Ile  
 145 150 155 160

Thr Tyr Ile Glu Ile Leu Ala Glu Ser Ser Ser Leu Leu Gly Tyr Lys  
165 170 175

Asn Asn Thr Ile Ser Ala Lys Asp Thr Leu Ser Asn Ser Thr Leu Thr

180	185	190
Glu Phe Val Lys Thr Val Asn Asn Phe Val Gln Arg Asp Thr Phe Val		
195	200	205
Val Trp Asp Lys Leu Ser Val Asn His Arg Arg Thr His Leu Thr Lys		
210	215	220
Leu Met His Thr Val Glu Gln Ala Thr Leu Arg Ile Ser Gln Ser Phe		
225	230	235
Gln Lys Thr Thr Glu Phe Asp Thr Asn Ser Thr Asp Ile Ala Leu Lys		
245	250	255
Val Phe Phe Phe Asp Ser Tyr Asn Met Lys His Ile His Pro His Met		
260	265	270
Asn Met Asp Gly Asp Tyr Ile Asn Ile Phe Pro Lys Arg Lys Ala Ala		
275	280	285
Tyr Asp Ser Asn Gly Asn Val Ala Val Ala Phe Leu Tyr Tyr Lys Ser		
290	295	300
Ile Gly Pro Leu Leu Ser Ser Asp Asn Phe Leu Leu Lys Pro Gln		
305	310	315
Asn Tyr Asp Asn Ser Glu Glu Glu Arg Val Ile Ser Ser Val Ile		
325	330	335
Ser Val Ser Met Ser Ser Asn Pro Pro Thr Leu Tyr Glu Leu Glu Lys		
340	345	350
Ile Thr Phe Thr Leu Ser His Arg Lys Val Thr Asp Arg Tyr Arg Ser		
355	360	365
Leu Cys Ala Phe Trp Asn Tyr Ser Pro Asp Thr Met Asn Gly Ser Trp		
370	375	380
Ser Ser Glu Gly Cys Glu Leu Thr Tyr Ser Asn Glu Thr His Thr Ser		
385	390	395
Cys Arg Cys Asn His Leu Thr His Phe Ala Ile Leu Met Ser Ser Gly		
405	410	415
Pro Ser Ile Gly Ile Lys Asp Tyr Asn Ile Leu Thr Arg Ile Thr Gln		
420	425	430
Leu Gly Ile Ile Ile Ser Leu Ile Cys Leu Ala Ile Cys Ile Phe Thr		
435	440	445
Phe Trp Phe Phe Ser Glu Ile Gln Ser Thr Arg Thr Thr Ile His Lys		
450	455	460

Asn Leu Cys Cys Ser Leu Phe Leu Ala Glu Leu Val Phe Leu Val Gly  
 465 470 475 480

Ile Asn Thr Asn Thr Asn Lys Leu Phe Cys Ser Ile Ile Ala Gly Leu  
 485 490 495

Leu His Tyr Phe Phe Leu Ala Ala Phe Ala Trp Met Cys Ile Glu Gly  
 500 505 510

Ile His Leu Tyr Leu Ile Val Val Gly Val Ile Tyr Asn Lys Gly Phe  
 515 520 525

Leu His Lys Asn Phe Tyr Ile Phe Gly Tyr Leu Ser Pro Ala Val Val  
 530 535 540

Val Gly Phe Ser Ala Ala Leu Gly Tyr Arg Tyr Tyr Gly Thr Thr Lys  
 545 550 555 560

Val Cys Trp Leu Ser Thr Glu Asn Asn Phe Ile Trp Ser Phe Ile Gly  
 565 570 575

Pro Ala Cys Leu Ile Ile Leu Val Asn Leu Leu Ala Phe Gly Val Ile  
 580 585 590

Ile Tyr Lys Val Phe Arg His Thr Ala Gly Leu Lys Pro Glu Val Ser  
 595 600 605

Cys Phe Glu Asn Ile Arg Ser Cys Ala Arg Gly Ala Leu Ala Leu Leu  
 610 615 620

Phe Leu Leu Gly Thr Thr Trp Ile Phe Gly Val Leu His Val Val His  
 625 630 635 640

Ala Ser Val Val Thr Ala Tyr Leu Phe Thr Val Ser Asn Ala Phe Gln  
 645 650 655

Gly Met Phe Ile Phe Leu Phe Leu Cys Val Leu Ser Arg Lys Ile Gln  
 660 665 670

Glu Glu Tyr Tyr Arg Leu Phe Lys Asn Val Pro Cys Cys Phe Gly Cys  
 675 680 685

Leu Arg  
 690

<210> 50  
 <211> 589  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> modified\_base  
 <222> (61)

<223> a, t, c or g

<400> 50

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ngaaaagccg gcataatggat tcaaattggca atgttgcagt tgcatttta tattataaga 120  
gtattggtcc cttgcatttc atcatctgac aacttcttat tgaaacctca aaattatgat 180  
aattctgaag aggagggaaag agtcataatct tcaagtaattt cagtcataat gagctcaaac 240  
ccacccacat tatataact tgaaaaaaata acatttacat taagtcatacg aaaggtcaca 300  
gataggtata ggagtctatg tggcattttg gaataactcac ctgataccat gaatggcagc 360  
tggcttcag agggctgtga gctgacatac tcaaattgaga cccacacctc atgccgtgt 420  
aatcacctga cacatttgc aattttgatg tcctctggc cttccattgg tattaaagat 480  
tataatattc ttacaaggat cactcaacta gaaataatta tttcaactgat ttgtcttgcc 540  
atatgcattt ttaccttctg gttcttcagt gaaattcaaa gcaccagga 589

<210> 51

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 51

ggtaatgagc tccattacag

20

<210> 52

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 52

ggagtagaaa gcgcattgg

18

<210> 53

<211> 22

<212> DNA

### <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 53

cacctgatac catgaatggc ag

22

<210> 54

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 54

cgagctcgaa ttaattcg

18

<210> 55

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 55

ggatctcctg agtcagg

18

<210> 56

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 56

cctagtttag tgatccttgt aag

23

<210> 57

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 57

atgagaccca cacctcatgc cgctgtaatc acctgacaca ttttgcatt

50

<210> 58

<211> 2137

<212> DNA

<213> Homo sapiens

<400> 58

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cgctaaggca ggcctcctcc tcccgagat ccgaacggcc tgggcggggt caccggct 120

gggacaaga gcccgcgcct gcctgcccgg gcccggggag ggggctgggg ctggggccgg 180  
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tgctcggtg tttgggcac ctaccgtgg gccccgttaag ggcgtactat ataaggctgc 300  
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<210> 59  
<211> 216  
<212> PRT  
<213> *Homo sapiens*

<400> 59

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20 25 30

His Val His Tyr Gly Trp Gly Asp Pro Ile Arg Leu Arg His Leu Tyr  
                  35                 40                 45

Thr Ser Gly Pro His Gly Leu Ser Ser Cys Phe Leu Arg Ile Arg Ala  
50 55 60

Asp Gly Val Val Asp Cys Ala Arg Gly Gln Ser Ala His Ser Leu Leu  
 65 70 75 80

Glu Ile Lys Ala Val Ala Leu Arg Thr Val Ala Ile Lys Gly Val His  
 85 90 95

Ser Val Arg Tyr Leu Cys Met Gly Ala Asp Gly Lys Met Gln Gly Leu  
 100 105 110

Leu Gln Tyr Ser Glu Glu Asp Cys Ala Phe Glu Glu Glu Ile Arg Pro  
 115 120 125

Asp Gly Tyr Asn Val Tyr Arg Ser Glu Lys His Arg Leu Pro Val Ser  
 130 135 140

Leu Ser Ser Ala Lys Gln Arg Gln Leu Tyr Lys Asn Arg Gly Phe Leu  
 145 150 155 160

Pro Leu Ser His Phe Leu Pro Met Leu Pro Met Val Pro Glu Glu Pro  
 165 170 175

Glu Asp Leu Arg Gly His Leu Glu Ser Asp Met Phe Ser Ser Pro Leu  
 180 185 190

Glu Thr Asp Ser Met Asp Pro Phe Gly Leu Val Thr Gly Leu Glu Ala  
 195 200 205

Val Arg Ser Pro Ser Phe Glu Lys  
 210 215

<210> 60  
 <211> 26  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 60  
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<210> 61  
 <211> 42  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 61  
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<210> 62
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe

<400> 62
ccagtccgt gacaagccca aa 22

<210> 63
<211> 1295
<212> DNA
<213> Homo sapiens

<400> 63
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<210> 64
<211> 312
<212> PRT
<213> Homo sapiens

<400> 64
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Leu Val Val Ala Leu Gly Tyr His Lys Ala Tyr Gly Phe Ser Ala Pro
   20          25          30

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Lys Asp Gln Gln Val Val Thr Ala Val Glu Tyr Gln Glu Ala Ile Leu  
                   35                        40                          45  
 Ala Cys Lys Thr Pro Lys Lys Thr Val Ser Ser Arg Leu Glu Trp Lys  
                   50                        55                        60  
 Lys Leu Gly Arg Ser Val Ser Phe Val Tyr Tyr Gln Gln Thr Leu Gln  
                   65                        70                        75                  80  
 Gly Asp Phe Lys Asn Arg Ala Glu Met Ile Asp Phe Asn Ile Arg Ile  
                   85                        90                        95  
 Lys Asn Val Thr Arg Ser Asp Ala Gly Lys Tyr Arg Cys Glu Val Ser  
                   100                       105                       110  
 Ala Pro Ser Glu Gln Gly Gln Asn Leu Glu Glu Asp Thr Val Thr Leu  
                   115                       120                       125  
 Glu Val Leu Val Ala Pro Ala Val Pro Ser Cys Glu Val Pro Ser Ser  
                   130                       135                       140  
 Ala Leu Ser Gly Thr Val Val Glu Leu Arg Cys Gln Asp Lys Glu Gly  
                   145                       150                       155                  160  
 Asn Pro Ala Pro Glu Tyr Thr Trp Phe Lys Asp Gly Ile Arg Leu Leu  
                   165                       170                       175  
 Glu Asn Pro Arg Leu Gly Ser Gln Ser Thr Asn Ser Ser Tyr Thr Met  
                   180                       185                       190  
 Asn Thr Lys Thr Gly Thr Leu Gln Phe Asn Thr Val Ser Lys Leu Asp  
                   195                       200                       205  
 Thr Gly Glu Tyr Ser Cys Glu Ala Arg Asn Ser Val Gly Tyr Arg Arg  
                   210                       215                       220  
 Cys Pro Gly Lys Arg Met Gln Val Asp Asp Leu Asn Ile Ser Gly Ile  
                   225                       230                       235                  240  
 Ile Ala Ala Val Val Val Val Ala Leu Val Ile Ser Val Cys Gly Leu  
                   245                       250                       255  
 Gly Val Cys Tyr Ala Gln Arg Lys Gly Tyr Phe Ser Lys Glu Thr Ser  
                   260                       265                       270  
 Phe Gln Lys Ser Asn Ser Ser Ser Lys Ala Thr Thr Met Ser Glu Asn  
                   275                       280                       285  
 Val Gln Trp Leu Thr Pro Val Ile Pro Ala Leu Trp Lys Ala Ala Ala  
                   290                       295                       300  
 Gly Gly Ser Arg Gly Gln Glu Phe

305

310

<210> 65  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 65  
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22

<210> 66  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 66  
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23

<210> 67  
<211> 48  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 67  
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48

<210> 68  
<211> 2639  
<212> DNA  
<213> Homo sapiens

<400> 68  
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gcatcatgtct gctattcctg caaatactga agaagcatgg gatttaaata ttttacttct 180  
aaataaaatga attactcaat ctccatgtac catctataca tactccacct tcaaaaagta 240  
catcaatatt atatcattaa ggaatagta accttctt ctccaatatgt catgacattt 300  
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tggcattcat catttgacaa atgcaagcat cttccttatac aatcagctcc tattgaactt 420  
actagcactg actgtggaat ccttaagggc ccattacatt tctgaagaag aaagctaaga 480  
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aagctgtaga taaaaaagtg gattgtccac ggttatgtac gtgtgaaatc aggccctgg 600  
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 taaatctctg ggaaggcagga aaagaaaaaa gtacatcact gaaagtaaaa gcaactgtta 2580  
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<210> 69  
 <211> 708  
 <212> PRT  
 <213> Homo sapiens

<400> 69  
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Cys Thr Cys Glu Ile Arg Pro Trp Phe Thr Pro Arg Ser Ile Tyr Met  
 35 40 45

Glu Ala Ser Thr Val Asp Cys Asn Asp Leu Gly Leu Leu Thr Phe Pro  
 50 55 60

Ala Arg Leu Pro Ala Asn Thr Gln Ile Leu Leu Leu Gln Thr Asn Asn  
 65 70 75 80  
 Ile Ala Lys Ile Glu Tyr Ser Thr Asp Phe Pro Val Asn Leu Thr Gly  
 85 90 95  
 Leu Asp Leu Ser Gln Asn Asn Leu Ser Ser Val Thr Asn Ile Asn Val  
 100 105 110  
 Lys Lys Met Pro Gln Leu Leu Ser Val Tyr Leu Glu Glu Asn Lys Leu  
 115 120 125  
 Thr Glu Leu Pro Glu Lys Cys Leu Ser Glu Leu Ser Asn Leu Gln Glu  
 130 135 140  
 Leu Tyr Ile Asn His Asn Leu Leu Ser Thr Ile Ser Pro Gly Ala Phe  
 145 150 155 160  
 Ile Gly Leu His Asn Leu Leu Arg Leu His Leu Asn Ser Asn Arg Leu  
 165 170 175  
 Gln Met Ile Asn Ser Lys Trp Phe Asp Ala Leu Pro Asn Leu Glu Ile  
 180 185 190  
 Leu Met Ile Gly Glu Asn Pro Ile Ile Arg Ile Lys Asp Met Asn Phe  
 195 200 205  
 Lys Pro Leu Ile Asn Leu Arg Ser Leu Val Ile Ala Gly Ile Asn Leu  
 210 215 220  
 Thr Glu Ile Pro Asp Asn Ala Leu Val Gly Leu Glu Asn Leu Glu Ser  
 225 230 235 240  
 Ile Ser Phe Tyr Asp Asn Arg Leu Ile Lys Val Pro His Val Ala Leu  
 245 250 255  
 Gln Lys Val Val Asn Leu Lys Phe Leu Asp Leu Asn Lys Asn Pro Ile  
 260 265 270  
 Asn Arg Ile Arg Arg Gly Asp Phe Ser Asn Met Leu His Leu Lys Glu  
 275 280 285  
 Leu Gly Ile Asn Asn Met Pro Glu Leu Ile Ser Ile Asp Ser Leu Ala  
 290 295 300  
 Val Asp Asn Leu Pro Asp Leu Arg Lys Ile Glu Ala Thr Asn Asn Pro  
 305 310 315 320  
 Arg Leu Ser Tyr Ile His Pro Asn Ala Phe Phe Arg Leu Pro Lys Leu  
 325 330 335  
 Glu Ser Leu Met Leu Asn Ser Asn Ala Leu Ser Ala Leu Tyr His Gly

340	345	350
Thr Ile Glu Ser Leu Pro Asn Leu Lys Glu Ile Ser Ile His Ser Asn		
355	360	365
Pro Ile Arg Cys Asp Cys Val Ile Arg Trp Met Asn Met Asn Lys Thr		
370	375	380
Asn Ile Arg Phe Met Glu Pro Asp Ser Leu Phe Cys Val Asp Pro Pro		
385	390	395
Glu Phe Gln Gly Gln Asn Val Arg Gln Val His Phe Arg Asp Met Met		
405	410	415
Glu Ile Cys Leu Pro Leu Ile Ala Pro Glu Ser Phe Pro Ser Asn Leu		
420	425	430
Asn Val Glu Ala Gly Ser Tyr Val Ser Phe His Cys Arg Ala Thr Ala		
435	440	445
Glu Pro Gln Pro Glu Ile Tyr Trp Ile Thr Pro Ser Gly Gln Lys Leu		
450	455	460
Leu Pro Asn Thr Leu Thr Asp Lys Phe Tyr Val His Ser Glu Gly Thr		
465	470	475
Leu Asp Ile Asn Gly Val Thr Pro Lys Glu Gly Gly Leu Tyr Thr Cys		
485	490	495
Ile Ala Thr Asn Leu Val Gly Ala Asp Leu Lys Ser Val Met Ile Lys		
500	505	510
Val Asp Gly Ser Phe Pro Gln Asp Asn Asn Gly Ser Leu Asn Ile Lys		
515	520	525
Ile Arg Asp Ile Gln Ala Asn Ser Val Leu Val Ser Trp Lys Ala Ser		
530	535	540
Ser Lys Ile Leu Lys Ser Ser Val Lys Trp Thr Ala Phe Val Lys Thr		
545	550	555
Glu Asn Ser His Ala Ala Gln Ser Ala Arg Ile Pro Ser Asp Val Lys		
565	570	575
Val Tyr Asn Leu Thr His Leu Asn Pro Ser Thr Glu Tyr Lys Ile Cys		
580	585	590
Ile Asp Ile Pro Thr Ile Tyr Gln Lys Asn Arg Lys Lys Cys Val Asn		
595	600	605
Val Thr Thr Lys Gly Leu His Pro Asp Gln Lys Glu Tyr Glu Lys Asn		
610	615	620

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Asn	Thr	Thr	Thr	Leu	Met	Ala	Cys	Leu	Gly	Gly	Leu	Leu	Gly	Ile	Ile
625														640	
															635
Gly	Val	Ile	Cys	Leu	Ile	Ser	Cys	Leu	Ser	Pro	Glu	Met	Asn	Cys	Asp
														655	
															645
															650
Gly	Gly	His	Ser	Tyr	Val	Arg	Asn	Tyr	Leu	Gln	Lys	Pro	Thr	Phe	Ala
															670
															660
Leu	Gly	Glu	Leu	Tyr	Pro	Pro	Leu	Ile	Asn	Leu	Trp	Glu	Ala	Gly	Lys
															685
															675
Glu	Lys	Ser	Thr	Ser	Leu	Lys	Val	Lys	Ala	Thr	Val	Ile	Gly	Leu	Pro
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															690

Thr Asn Met Ser  
705

<210> 70  
<211> 1305  
<212> DNA  
<213> Homo sapiens

<400> 70  
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ttaccacgct ttttggagta gatgaggaat gggctcgta ttatgctgac attccagcat 180  
gaatctggta gacctgtgtt taacccgttc cctctccatg tgcctcctcc tacaaagttt 240  
ttttctttag atactgtgtt ttcattctgc cagtatgtgtt cccaaagggtt gtctttgttc 300  
ttccctctggg ggtttaaatg tcacctgttag caatgcaaat ctcaaggaaa tacctagaga 360  
tcttcctccat gaaacagtct tactgtatct ggactccaat cagatcacat ctattcccaa 420  
tgaaatttttt aaggacctcc atcaactgttag agttctcaac ctgtccaaaaa atggcattga 480  
gtttatcgat gagcatgcct tcaaaggagt agctgaaacc ttgcagactc tggacttg 540  
cgacaatcggtt attcaagtg tgcacaaaaaa tgcctcaat aacctgaagg ccaggccag 600  
aattgccaac aacccctggc actgcgactg tactctacag caagttctga ggagcatggc 660  
gtccaaatcat gagacagccc acaacgtgtt ctgtaaaaacg tccgtgttgg atgaacatgc 720  
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taccgattat gccatgtgg tcaccatgtt tggctgggtt actatgggtt tctcatatgt 840  
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cctgccaaggc aggccagaaga aagccagatga acctgtatgtt attacactg tggatagtg 960  
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caccccttaa ttgtacccccc gatggatat ttctgagtaa gctactatct gaacatttagt 1200  
tagatccatc tcactattta ataatgaaat ttatTTTTT aattttaaaag caaataaaaag 1260  
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<210> 71  
<211> 259  
<212> PRT  
<213> Homo sapiens

<400> 71

Met Asn Leu Val Asp Leu Trp Leu Thr Arg Ser Leu Ser Met Cys Leu  
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Leu Leu Gln Ser Phe Val Leu Met Ile Leu Cys Phe His Ser Ala Ser  
 20 25 30

Met Cys Pro Lys Gly Cys Leu Cys Ser Ser Ser Gly Gly Leu Asn Val  
 35 40 45

Thr Cys Ser Asn Ala Asn Leu Lys Glu Ile Pro Arg Asp Leu Pro Pro  
 50 55 60

Glu Thr Val Leu Leu Tyr Leu Asp Ser Asn Gln Ile Thr Ser Ile Pro  
 65 70 75 80

Asn Glu Ile Phe Lys Asp Leu His Gln Leu Arg Val Leu Asn Leu Ser  
 85 90 95

Lys Asn Gly Ile Glu Phe Ile Asp Glu His Ala Phe Lys Gly Val Ala  
 100 105 110

Glu Thr Leu Gln Thr Leu Asp Leu Ser Asp Asn Arg Ile Gln Ser Val  
 115 120 125

His Lys Asn Ala Phe Asn Asn Leu Lys Ala Arg Ala Arg Ile Ala Asn  
 130 135 140

Asn Pro Trp His Cys Asp Cys Thr Leu Gln Gln Val Leu Arg Ser Met  
 145 150 155 160

Ala Ser Asn His Glu Thr Ala His Asn Val Ile Cys Lys Thr Ser Val  
 165 170 175

Leu Asp Glu His Ala Gly Arg Pro Phe Leu Asn Ala Ala Asn Asp Ala  
 180 185 190

Asp Leu Cys Asn Leu Pro Lys Lys Thr Thr Asp Tyr Ala Met Leu Val  
 195 200 205

Thr Met Phe Gly Trp Phe Thr Met Val Ile Ser Tyr Val Val Tyr Tyr  
 210 215 220

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Val Arg Gln Asn Gln Glu Asp Ala Arg Arg His Leu Glu Tyr Leu Lys  
 225 230 235 240

Ser Leu Pro Ser Arg Gln Lys Lys Ala Asp Glu Pro Asp Asp Ile Ser  
 245 250 255

Thr Val Val

&lt;210&gt; 72

&lt;211&gt; 2290

<212> DNA  
<213> *Homo sapiens*

<400> 72

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ggggcgtagag gagcatgccc agccccctcc tggcctgctg gcagccatc ctccctgctgg 120  
tgctggctc agtgctgtca ggctcgccca cgggctgccc gccccctgc gagtgctccg 180  
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ccaccgagac ggcctgtctg gacctaggca agaaccgcata caaaaacgcata aaccaggacg 300  
agttcggccag ctccccgcac ctggaggagc tggagctcaa cgagaacatc gtgagcgcgg 360  
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gcctgaagct catcccgtca ggcgtcttca ctggcctcag caacctgacc aagcaggaca 480  
tcagcgagaa caagatcgat atcctactgg actacatgtt tcaggacctg tacaacctca 540  
agtcacttggaa ggttggcgac aatgacctcg tctacatctc tcaccgcgcc ttcagcggcc 600  
tcaacagcct ggagcagctg acgctggaga aatgcaacct gacccatc cccaccgagg 660  
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tccgggacta ctccttcaag aggctgtacc gactcaaggt ctggagatc tcccactg 780  
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aaaaaaaaaa 2290

<210> 73

<211> 620

<212> PRT

<213> Homo sapiens

<400> 73

Met Gln V

1

1

5

10

15

Ser Pro Leu Leu Ala Cys Trp Gln Pro Ile Leu Leu Leu Val Leu Gly  
           20                     25                     30

Ser Val Leu Ser Gly Ser Ala Thr Gly Cys Pro Pro Arg Cys Glu Cys  
           35                     40                     45

Ser Ala Gln Asp Arg Ala Val Leu Cys His Arg Lys Cys Phe Val Ala  
           50                     55                     60

Val Pro Glu Gly Ile Pro Thr Glu Thr Arg Leu Leu Asp Leu Gly Lys  
           65                     70                     75                     80

Asn Arg Ile Lys Thr Leu Asn Gln Asp Glu Phe Ala Ser Phe Pro His  
           85                     90                     95

Leu Glu Glu Leu Glu Leu Asn Glu Asn Ile Val Ser Ala Val Glu Pro  
           100                    105                     110

Gly Ala Phe Asn Asn Leu Phe Asn Leu Arg Thr Leu Gly Leu Arg Ser  
           115                    120                     125

Asn Arg Leu Lys Leu Ile Pro Leu Gly Val Phe Thr Gly Leu Ser Asn  
           130                    135                     140

Leu Thr Lys Gln Asp Ile Ser Glu Asn Lys Ile Val Ile Leu Leu Asp  
           145                    150                     155                     160

Tyr Met Phe Gln Asp Leu Tyr Asn Leu Lys Ser Leu Glu Val Gly Asp  
           165                    170                     175

Asn Asp Leu Val Tyr Ile Ser His Arg Ala Phe Ser Gly Leu Asn Ser  
           180                    185                     190

Leu Glu Gln Leu Thr Leu Glu Lys Cys Asn Leu Thr Ser Ile Pro Thr  
           195                    200                     205

Glu Ala Leu Ser His Leu His Gly Leu Ile Val Leu Arg Leu Arg His  
           210                    215                     220

Leu Asn Ile Asn Ala Ile Arg Asp Tyr Ser Phe Lys Arg Leu Tyr Arg  
           225                    230                     235                     240

Leu Lys Val Leu Glu Ile Ser His Trp Pro Tyr Leu Asp Thr Met Thr  
           245                    250                     255

Pro Asn Cys Leu Tyr Gly Leu Asn Leu Thr Ser Leu Ser Ile Thr His  
           260                    265                     270

Cys Asn Leu Thr Ala Val Pro Tyr Leu Ala Val Arg His Leu Val Tyr  
           275                    280                     285

Leu Arg Phe Leu Asn Leu Ser Tyr Asn Pro Ile Ser Thr Ile Glu Gly  
           290                    295                     300

Ser Met Leu His Glu Leu Leu Arg Leu Gln Glu Ile Gln Leu Val Gly  
 305 310 315 320

Gly Gln Leu Ala Val Val Glu Pro Tyr Ala Phe Arg Gly Leu Asn Tyr  
 325 330 335

Leu Arg Val Leu Asn Val Ser Gly Asn Gln Leu Thr Thr Leu Glu Glu  
 340 345 350

Ser Val Phe His Ser Val Gly Asn Leu Glu Thr Leu Ile Leu Asp Ser  
 355 360 365

Asn Pro Leu Ala Cys Asp Cys Arg Leu Leu Trp Val Phe Arg Arg Arg  
 370 375 380

Trp Arg Leu Asn Phe Asn Arg Gln Gln Pro Thr Cys Ala Thr Pro Glu  
 385 390 395 400

Phe Val Gln Gly Lys Glu Phe Lys Asp Phe Pro Asp Val Leu Leu Pro  
 405 410 415

Asn Tyr Phe Thr Cys Arg Arg Ala Arg Ile Arg Asp Arg Lys Ala Gln  
 420 425 430

Gln Val Phe Val Asp Glu Gly His Thr Val Gln Phe Val Cys Arg Ala  
 435 440 445

Asp Gly Asp Pro Pro Pro Ala Ile Leu Trp Leu Ser Pro Arg Lys His  
 450 455 460

Leu Val Ser Ala Lys Ser Asn Gly Arg Leu Thr Val Phe Pro Asp Gly  
 465 470 475 480

Thr Leu Glu Val Arg Tyr Ala Gln Val Gln Asp Asn Gly Thr Tyr Leu  
 485 490 495

Cys Ile Ala Ala Asn Ala Gly Gly Asn Asp Ser Met Pro Ala His Leu  
 500 505 510

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His Val Arg Ser Tyr Ser Pro Asp Trp Pro His Gln Pro Asn Lys Thr  
 515 520 525

Phe Ala Phe Ile Ser Asn Gln Pro Gly Glu Gly Ala Asn Ser Thr  
 530 535 540

Arg Ala Thr Val Pro Phe Pro Phe Asp Ile Lys Thr Leu Ile Ile Ala  
 545 550 555 560

Thr Thr Met Gly Phe Ile Ser Phe Leu Gly Val Val Leu Phe Cys Leu  
 565 570 575

Val Leu Leu Phe Leu Trp Ser Arg Gly Lys Gly Asn Thr Lys His Asn

580	585	590
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595	600	605
Ala Asp Ala Pro Arg Lys Phe Asn Met Lys Met Ile		
610	615	620
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<211> 22		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe		
<400> 74		
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22		
<210> 75		
<211> 23		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe		
<400> 75		
ataccagcta taaccaggct gcg		
23		
<210> 76		
<211> 52		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe		
<400> 76		
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50		
gg		
52		
<210> 77		
<211> 22		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe		

<400> 77  
ccatgtgtct cctcctacaa ag 22

<210> 78  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 78  
ggaaatagat gtgatctgat tgg 23

<210> 79  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 79  
cacctgttagc aatgcaaatc tcaaggaaat acctagagat cttcctcctg 50

<210> 80  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 80  
agcaaccgcc tgaagctcat cc 22

<210> 81  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 81  
aaggcgccgtt gaaagatgtt gacg 24

<210> 82

<211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 82  
 gactacatgt ttcaggacct gtacaacctc aagtcaactgg aggttggcga 50

<210> 83  
 <211> 1685  
 <212> DNA  
 <213> Homo sapiens

<400> 83  
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 agccaggagg cccggccggga agcgcgatgg gggcccccagc cgcctcgctc ctgctcctgc 180  
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 tgaaaagatca cgaggactca tccctgcaat ggtctaaccct tgctcagcag actctctact 360  
 ttggggagaa gagagccctt cgagataatc gaattcagct ggtaacctt acgc(cc)acg 420  
 agctcagcat cagcatcagc aatgtggccc tggcagacga gggcgagttac acctgctcaa 480  
 ttttcactat gcctgtgcga actgccaagt ccctcgctc tgctcgttaga attccacaga 540  
 agccatcat cactggttat aaatcttcat tacggaaaa agacacagcc accctaaact 600  
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 ccccttcgt ggcttcgtt cattgggtt attattattt ttgtaaataat cccaaatcaa 1620  
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 aaaca 1685

<210> 84  
 <211> 398  
 <212> PRT  
 <213> Homo sapiens

<400> 84

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Pro Trp Thr Ser Asp Glu Thr Val Val Ala Gly Gly Thr Val Val Leu  
 35 40 45

Lys Cys Gln Val Lys Asp His Glu Asp Ser Ser Leu Gln Trp Ser Asn  
 50 55 60

Pro Ala Gln Gln Thr Leu Tyr Phe Gly Glu Lys Arg Ala Leu Arg Asp  
 65 70 75 80

Asn Arg Ile Gln Leu Val Thr Ser Thr Pro His Glu Leu Ser Ile Ser  
 85 90 95

Ile Ser Asn Val Ala Leu Ala Asp Glu Gly Glu Tyr Thr Cys Ser Ile  
 100 105 110

Phe Thr Met Pro Val Arg Thr Ala Lys Ser Leu Val Thr Val Leu Gly  
 115 120 125

Ile Pro Gln Lys Pro Ile Ile Thr Gly Tyr Lys Ser Ser Leu Arg Glu  
 130 135 140

Lys Asp Thr Ala Thr Leu Asn Cys Gln Ser Ser Gly Ser Lys Pro Ala  
 145 150 155 160

Ala Arg Leu Thr Trp Arg Lys Gly Asp Gln Glu Leu His Gly Glu Pro  
 165 170 175

Thr Arg Ile Gln Glu Asp Pro Asn Gly Lys Thr Phe Thr Val Ser Ser  
 180 185 190

Ser Val Thr Phe Gln Val Thr Arg Glu Asp Asp Gly Ala Ser Ile Val  
 195 200 205

Cys Ser Val Asn His Glu Ser Leu Lys Gly Ala Asp Arg Ser Thr Ser  
 210 215 220

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Gln Arg Ile Glu Val Leu Tyr Thr Pro Thr Ala Met Ile Arg Pro Asp  
 225 230 235 240

Pro Pro His Pro Arg Glu Gly Gln Lys Leu Leu Leu His Cys Glu Gly  
 245 250 255

Arg Gly Asn Pro Val Pro Gln Gln Tyr Leu Trp Glu Lys Glu Gly Ser  
 260 265 270

Val Pro Pro Leu Lys Met Thr Gln Glu Ser Ala Leu Ile Phe Pro Phe  
 275 280 285

Leu Asn Lys Ser Asp Ser Gly Thr Tyr Gly Cys Thr Ala Thr Ser Asn  
290 295 300

Met Gly Ser Tyr Lys Ala Tyr Tyr Thr Leu Asn Val Asn Asp Pro Ser  
305 310 315 320

Pro Val Pro Ser Ser Ser Thr Tyr His Ala Ile Ile Gly Gly Ile  
325 330 335

Val Ala Phe Ile Val Phe Leu Leu Leu Ile Met Leu Ile Phe Leu Gly  
340 345 350

His Tyr Leu Ile Arg His Lys Gly Thr Tyr Leu Thr His Glu Ala Lys  
355 360 365

Gly Ser Asp Asp Ala Pro Asp Ala Asp Thr Ala Ile Ile Asn Ala Glu  
370 375 380

Gly Gly Gln Ser Gly Gly Asp Asp Lys Lys Glu Tyr Phe Ile  
385 390 395

<210> 85

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 85

gcttagaatt ccacagaagc cc

22

<210> 86

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 86

aacctggaaat gtcaccgagc tg

22

<210> 87

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

## oligonucleotide probe

<400> 87  
 cctagcacag tgacgaggga ctggc 26

<210> 88  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 88  
 aagacacagc caccctaaac tgtcagtctt ctgggagcaa gcctgcagcc 50

<210> 89  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 89  
 gccctggcag acgagggcga gtacacctgc tcaatcttca ctatgcctgt 50

<210> 90  
 <211> 2755  
 <212> DNA  
 <213> Homo sapiens

<400> 90  
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<210> 91  
 <211> 696  
 <212> PRT  
 <213> Homo sapiens

<400> 91  
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 20 25 30

Glu Ile Glu Gly Asp Leu His Val Asp Cys Glu Lys Lys Gly Phe Thr  
 35 40 45

Ser Leu Gln Arg Phe Thr Ala Pro Thr Ser Gln Phe Tyr His Leu Phe  
 50 55 60

Leu His Gly Asn Ser Leu Thr Arg Leu Phe Pro Asn Glu Phe Ala Asn  
 65 70 75 80

Phe Tyr Asn Ala Val Ser Leu His Met Glu Asn Asn Gly Leu His Glu  
 85 90 95

Ile Val Pro Gly Ala Phe Leu Gly Leu Gln Leu Val Lys Arg Leu His  
 100 105 110  
 Ile Asn Asn Asn Lys Ile Lys Ser Phe Arg Lys Gln Thr Phe Leu Gly  
 115 120 125  
 Leu Asp Asp Leu Glu Tyr Leu Gln Ala Asp Phe Asn Leu Leu Arg Asp  
 130 135 140  
 Ile Asp Pro Gly Ala Phe Gln Asp Leu Asn Lys Leu Glu Val Leu Ile  
 145 150 155 160  
 Leu Asn Asp Asn Leu Ile Ser Thr Leu Pro Ala Asn Val Phe Gln Tyr  
 165 170 175  
 Val Pro Ile Thr His Leu Asp Leu Arg Gly Asn Arg Leu Lys Thr Leu  
 180 185 190  
 Pro Tyr Glu Glu Val Leu Glu Gln Ile Pro Gly Ile Ala Glu Ile Leu  
 195 200 205  
 Leu Glu Asp Asn Pro Trp Asp Cys Thr Cys Asp Leu Leu Ser Leu Lys  
 210 215 220  
 Glu Trp Leu Glu Asn Ile Pro Lys Asn Ala Leu Ile Gly Arg Val Val  
 225 230 235 240  
 Cys Glu Ala Pro Thr Arg Leu Gln Gly Lys Asp Leu Asn Glu Thr Thr  
 245 250 255  
 Glu Gln Asp Leu Cys Pro Leu Lys Asn Arg Val Asp Ser Ser Leu Pro  
 260 265 270  
 Ala Pro Pro Ala Gln Glu Glu Thr Phe Ala Pro Gly Pro Leu Pro Thr  
 275 280 285  
 Pro Phe Lys Thr Asn Gly Gln Glu Asp His Ala Thr Pro Gly Ser Ala  
 290 295 300  
 Pro Asn Gly Gly Thr Lys Ile Pro Gly Asn Trp Gln Ile Lys Ile Arg  
 305 310 315 320  
 Pro Thr Ala Ala Ile Ala Thr Gly Ser Ser Arg Asn Lys Pro Leu Ala  
 325 330 335  
 Asn Ser Leu Pro Cys Pro Gly Gly Cys Ser Cys Asp His Ile Pro Gly  
 340 345 350  
 Ser Gly Leu Lys Met Asn Cys Asn Asn Arg Asn Val Ser Ser Leu Ala  
 355 360 365  
 Asp Leu Lys Pro Lys Leu Ser Asn Val Gln Glu Leu Phe Leu Arg Asp  
 370 375 380

Asn Lys Ile His Ser Ile Arg Lys Ser His Phe Val Asp Tyr Lys Asn  
 385 390 395 400  
 Leu Ile Leu Leu Asp Leu Gly Asn Asn Asn Ile Ala Thr Val Glu Asn  
 405 410 415  
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 420 425 430  
 Asn Tyr Leu Asp Thr Leu Ser Arg Glu Lys Phe Ala Gly Leu Gln Asn  
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 450 455 460  
 Gly Thr Phe Asn Ala Met Pro Lys Leu Arg Ile Leu Ile Leu Asn Asn  
 465 470 475 480  
 Asn Leu Leu Arg Ser Leu Pro Val Asp Val Phe Ala Gly Val Ser Leu  
 485 490 495  
 Ser Lys Leu Ser Leu His Asn Asn Tyr Phe Met Tyr Leu Pro Val Ala  
 500 505 510  
 Gly Val Leu Asp Gln Leu Thr Ser Ile Ile Gln Ile Asp Leu His Gly  
 515 520 525  
 Asn Pro Trp Glu Cys Ser Cys Thr Ile Val Pro Phe Lys Gln Trp Ala  
 530 535 540  
 Glu Arg Leu Gly Ser Glu Val Leu Met Ser Asp Leu Lys Cys Glu Thr  
 545 550 555 560  
 Pro Val Asn Phe Phe Arg Lys Asp Phe Met Leu Leu Ser Asn Asp Glu  
 565 570 575  
 Ile Cys Pro Gln Leu Tyr Ala Arg Ile Ser Pro Thr Leu Thr Ser His  
 580 585 590  
 Ser Lys Asn Ser Thr Gly Leu Ala Glu Thr Gly Thr His Ser Asn Ser  
 595 600 605  
 Tyr Leu Asp Thr Ser Arg Val Ser Ile Ser Val Leu Val Pro Gly Leu  
 610 615 620  
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 625 630 635 640  
 Phe Ile Leu Arg Asn Arg Lys Arg Ser Lys Arg Arg Asp Ala Asn Ser  
 645 650 655  
 Ser Ala Ser Glu Ile Asn Ser Leu Gln Thr Val Cys Asp Ser Ser Tyr

660

665

670

Trp His Asn Gly Pro Tyr Asn Ala Asp Gly Ala His Arg Val Tyr Asp  
 675 680 685

Cys Gly Ser His Ser Leu Ser Asp  
 690 695

&lt;210&gt; 92

&lt;211&gt; 22

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 92

gttggatctg ggcaacaata ac

22

&lt;210&gt; 93

&lt;211&gt; 24

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 93

attgttgtgc aggctgagtt taag

24

&lt;210&gt; 94

&lt;211&gt; 45

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 94

ggtggtata catggatagc aattacctgg acacgctgtc ccggg

45

&lt;210&gt; 95

&lt;211&gt; 2226

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 95

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 aatttacatt aaaaaataat ttctaccaaa atggaaagga aatgttctat gttgttcagg 2160  
 ctaggatattggc aatcccaggg aaaaaataa aaataaaaaaa tttaaggatt 2220  
 gttgat 2226

<210> 96  
 <211> 490  
 <212> PRT  
 <213> Homo sapiens

<400> 96  
 Met Arg Pro Ala Phe Ala Leu Cys Leu Leu Trp Gln Ala Leu Trp Pro  
 1 5 10 15

Gly Pro Gly Gly Glu His Pro Thr Ala Asp Arg Ala Gly Cys Ser  
 20 25 30

Ala Ser Gly Ala Cys Tyr Ser Leu His His Ala Thr Met Lys Arg Gln  
 35 40 45

Ala Ala Glu Glu Ala Cys Ile Leu Arg Gly Gly Ala Leu Ser Thr Val  
 50 55 60

Arg Ala Gly Ala Glu Leu Arg Ala Val Leu Ala Leu Leu Arg Ala Gly  
 65 70 75 80  
 Pro Gly Pro Gly Gly Ser Lys Asp Leu Leu Phe Trp Val Ala Leu  
 85 90 95  
 Glu Arg Arg Arg Ser His Cys Thr Leu Glu Asn Glu Pro Leu Arg Gly  
 100 105 110  
 Phe Ser Trp Leu Ser Ser Asp Pro Gly Gly Leu Glu Ser Asp Thr Leu  
 115 120 125  
 Gln Trp Val Glu Glu Pro Gln Arg Ser Cys Thr Ala Arg Arg Cys Ala  
 130 135 140  
 Val Leu Gln Ala Thr Gly Gly Val Glu Pro Ala Gly Trp Lys Glu Met  
 145 150 155 160  
 Arg Cys His Leu Arg Ala Asn Gly Tyr Leu Cys Lys Tyr Gln Phe Glu  
 165 170 175  
 Val Leu Cys Pro Ala Pro Arg Pro Gly Ala Ala Ser Asn Leu Ser Tyr  
 180 185 190  
 Arg Ala Pro Phe Gln Leu His Ser Ala Ala Leu Asp Phe Ser Pro Pro  
 195 200 205  
 Gly Thr Glu Val Ser Ala Leu Cys Arg Gly Gln Leu Pro Ile Ser Val  
 210 215 220  
 Thr Cys Ile Ala Asp Glu Ile Gly Ala Arg Trp Asp Lys Leu Ser Gly  
 225 230 235 240  
 Asp Val Leu Cys Pro Cys Pro Gly Arg Tyr Leu Arg Ala Gly Lys Cys  
 245 250 255  
 Ala Glu Leu Pro Asn Cys Leu Asp Asp Leu Gly Gly Phe Ala Cys Glu  
 260 265 270  
 Cys Ala Thr Gly Phe Glu Leu Gly Lys Asp Gly Arg Ser Cys Val Thr  
 275 280 285  
 Ser Gly Glu Gly Gln Pro Thr Leu Gly Gly Thr Gly Val Pro Thr Arg  
 290 295 300  
 Arg Pro Pro Ala Thr Ala Thr Ser Pro Val Pro Gln Arg Thr Trp Pro  
 305 310 315 320  
 Ile Arg Val Asp Glu Lys Leu Gly Glu Thr Pro Leu Val Pro Glu Gln  
 325 330 335  
 Asp Asn Ser Val Thr Ser Ile Pro Glu Ile Pro Arg Trp Gly Ser Gln

340	345	350
Ser Thr Met Ser Thr Leu Gln Met Ser Leu Gln Ala Glu Ser Lys Ala		
355	360	365
Thr Ile Thr Pro Ser Gly Ser Val Ile Ser Lys Phe Asn Ser Thr Thr		
370	375	380
Ser Ser Ala Thr Pro Gln Ala Phe Asp Ser Ser Ser Ala Val Val Phe		
385	390	395
Ile Phe Val Ser Thr Ala Val Val Val Leu Val Ile Leu Thr Met Thr		
405	410	415
Val Leu Gly Leu Val Lys Leu Cys Phe His Glu Ser Pro Ser Ser Gln		
420	425	430
Pro Arg Lys Glu Ser Met Gly Pro Pro Gly Leu Glu Ser Asp Pro Glu		
435	440	445
Pro Ala Ala Leu Gly Ser Ser Ser Ala His Cys Thr Asn Asn Gly Val		
450	455	460
Lys Val Gly Asp Cys Asp Leu Arg Asp Arg Ala Glu Gly Ala Leu Leu		
465	470	475
Ala Glu Ser Pro Leu Gly Ser Ser Asp Ala		
485	490	

<210> 97

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 97

tggaaggaga tgcgtatgcc a cctg

24

<210> 98

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 98

tgaccagtgg ggaaggacag

20

<210> 99  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 99  
acagagcaga ggggccttg 20

<210> 100  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 100  
tcagggacaa gtgggtctc tccc 24

<210> 101  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 101  
tcagggagg agtgtgcagt tctg 24

<210> 102  
<211> 50  
<212> DNA  
<213> Artificial Sequence

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<220>  
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 102  
acagctcccg atctcagtta cttgcattgc ggacgaaatc ggcgctcgct 50

<210> 103  
<211> 2026  
<212> DNA  
<213> Homo sapiens

<400> 103  
cggacgcgtg ggattcagca gtggccctgtg gctgccagag cagctcctca ggggaaacta 60  
agcgtcgagt cagacggcac cataatcgcc tttaaaaagtg cctccgcct gccggccgc 120  
tatccccgg ctacctggc cggcccccggg cggtgcgcgc gttagagggg ggcgcgggc 180  
agccgagcgc cgggtgtgagc cagcgtcgct gccagtgtga gcggcgggtg gagcgcgggt 240  
ggtgcggagg ggggtgtgtg cggcgcgcgc cggcgtgggg tgcaaaccac gagcgtctac 300  
gctgccatga ggggcgcgaa cgcctggcg ccactctgc tgctgctggc tgccgcacc 360  
cagctctcgc ggcagcagtc cccagagaga cctgtttca catgtgggtg cattcttact 420  
ggagagctg gatttattgg cagtgaaggt ttcctggag tgtaccctc aaatagcaaa 480  
tgtacttggaa aatcacagt tcccgaagga aaagtagtgc ttctcaattt ccgattcata 540  
gacctcgaga gtgacaacact gtgccgtat gactttgtgg atgtgtacaa tggccatgcc 600  
aatggccagc gcattggccg cttctgtggc actttccggc ctggagccct tgggtccagt 660  
ggcaacaaga tggatgtgca gatgattct gatgccaaca cagctggcaa tggcttcatg 720  
gccatgttct ccgctgctga accaaacgaa agaggggatc agtattgtgg aggactcett 780  
gacagacctt cccgctcttt taaaaccccc aactggccag accgggatta ccctgcagga 840  
gtcacttggtg tgggcacat tggtagccca aagaatcagc ttatagaatt aaagtttgag 900  
aagtttgatg tggagcgaga taactactgc cgatatgatt atgtggctgt gtttaatggc 960  
ggggaaagtca acgatgctag aagaattggaa aagtattgtg gtgatagtcc acctgcgc 1020  
atgtgtctg agagaaatga acttcttatt cagttttat cagacttaag ttaactgca 1080  
gatgggtta ttggtcacta catattcagg caaaaaaaaac tgcctacaac tacagaacag 1140  
cctgtcacca ccacattccc tggtaaccacg ggtttaaaac ccaccgtggc cttgtgtcaa 1200  
caaaagtgtt gacggacggg gactctggag ggcaattatt gttcaagtga ctttgtattt 1260  
gcccggcactg ttatcacaac catcactcgc gatgggagtt tgcacccac agtctcgatc 1320  
atcaacatct acaaagagg aaatttggcg attcagcagg cgggcaagaa catgagtgcc 1380  
aggctgactg tcgtctgca gcaagtccct ctcctcagaa gaggtctaaa ttacattatt 1440  
atgggcacaa taggtgaaga tgggcgaggc aaaatcatgc caaacagctt tatcatgatg 1500  
ttcaagacca agaattcagaa gctcctggat gcctaaaaataaataagcaatg ttaacagtg 1560  
actgtgtcca ttaagctgt attctgccc tgcctttgaa agatctatgt tctctcagta 1620  
gaaaaaaaaa tacttataaa attacatatt ctgaaaagagg attccgaaag atgggactgg 1680  
ttgactcttc acatgatggc ggtatgaggc ctccgagata gctgaggggaa gttcttgcc 1740  
tgctgtcaga ggacgcgtca tctgattggaa aacctgcgcga cttagtgcgg tgataggaag 1800  
ctaaaagtgt caagcgttgc cagcttggaa gcgtttattt atacatctt gtaaaaggat 1860  
attttagaat tgagttgtgt gaagatgtca aaaaaagatt ttagaagtgc aatatttata 1920  
tggttatttg tttcaccttc aagccttgc cctgagggtg tacaatcttgc tcttgcgtt 1980  
tctaaatcaa tqcttaataa aatattttta aaggaaaaaaa aaaaaaa 2026

<210> 104

<211> 415

<212> PRT

<213> Homo sapiens

<400> 104

Met Arg Gly Ala Asn Ala Trp Ala Pro Leu Cys Leu Leu Leu Ala Ala  
1 5 10 15

Ala Thr Gln Leu Ser Arg Gln Gln Ser Pro Glu Arg Pro Val Phe Thr  
                  20                 25                 30

Cys Gly Gly Ile Leu Thr Gly Glu Ser Gly Phe Ile Gly Ser Glu Gly  
35 40 45

Phe Pro Gly Val Tyr Pro Pro Asn Ser Lys Cys Thr Trp Lys Ile Thr  
50 55 60

Val Pro Glu Gly Lys Val Val Val Leu Asn Phe Arg Phe Ile Asp Leu  
 65 70 75 80  
 Glu Ser Asp Asn Leu Cys Arg Tyr Asp Phe Val Asp Val Tyr Asn Gly  
 85 90 95  
 His Ala Asn Gly Gln Arg Ile Gly Arg Phe Cys Gly Thr Phe Arg Pro  
 100 105 110  
 Gly Ala Leu Val Ser Ser Gly Asn Lys Met Met Val Gln Met Ile Ser  
 115 120 125  
 Asp Ala Asn Thr Ala Gly Asn Gly Phe Met Ala Met Phe Ser Ala Ala  
 130 135 140  
 Glu Pro Asn Glu Arg Gly Asp Gln Tyr Cys Gly Leu Leu Asp Arg  
 145 150 155 160  
 Pro Ser Gly Ser Phe Lys Thr Pro Asn Trp Pro Asp Arg Asp Tyr Pro  
 165 170 175  
 Ala Gly Val Thr Cys Val Trp His Ile Val Ala Pro Lys Asn Gln Leu  
 180 185 190  
 Ile Glu Leu Lys Phe Glu Lys Phe Asp Val Glu Arg Asp Asn Tyr Cys  
 195 200 205  
 Arg Tyr Asp Tyr Val Ala Val Phe Asn Gly Gly Glu Val Asn Asp Ala  
 210 215 220  
 Arg Arg Ile Gly Lys Tyr Cys Gly Asp Ser Pro Pro Ala Pro Ile Val  
 225 230 235 240  
 Ser Glu Arg Asn Glu Leu Leu Ile Gln Phe Leu Ser Asp Leu Ser Leu  
 245 250 255  
 Thr Ala Asp Gly Phe Ile Gly His Tyr Ile Phe Arg Pro Lys Lys Leu  
 260 265 270  
 Pro Thr Thr Thr Glu Gln Pro Val Thr Thr Thr Phe Pro Val Thr Thr  
 275 280 285  
 Gly Leu Lys Pro Thr Val Ala Leu Cys Gln Gln Lys Cys Arg Arg Thr  
 290 295 300  
 Gly Thr Leu Glu Gly Asn Tyr Cys Ser Ser Asp Phe Val Leu Ala Gly  
 305 310 315 320  
 Thr Val Ile Thr Thr Ile Thr Arg Asp Gly Ser Leu His Ala Thr Val  
 325 330 335  
 Ser Ile Ile Asn Ile Tyr Lys Glu Gly Asn Leu Ala Ile Gln Gln Ala

340

345

350

Gly Lys Asn Met Ser Ala Arg Leu Thr Val Val Cys Lys Gln Cys Pro  
355 360 365

Leu Leu Arg Arg Gly Leu Asn Tyr Ile Ile Met Gly Gln Val Gly Glu  
370 375 380

Asp Gly Arg Gly Lys Ile Met Pro Asn Ser Phe Ile Met Met Phe Lys  
385 390 395 400

Thr Lys Asn Gln Lys Leu Leu Asp Ala Leu Lys Asn Lys Gln Cys  
405 410 415

<210> 105

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 105

ccgattcata gacctcgaga gt

22

<210> 106

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 106

gtcaaggagt cctccacaat ac

22

<210> 107

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 107

gtgtacaatg gccatgccaa tggccagcgc attggccgct tctgt

45

<210> 108

<211> 1838

<212> DNA

<213> Homo sapiens

<400> 108  
 cggacgcgtg ggcggacgcg tggcgcccc acggcgccc cgggctgggg cggtcgcttc 60  
 ttccctctcc gtggcctacg aggtccccca gcctggtaa agatggccc atggccccc 120  
 aaggccctag tcccagctgt gctctggggc ctcagctct tcctcaacct cccaggacct 180  
 atctggctcc agccctctcc acctccccag tcttctcccc cgccctcagcc ccattcgctgt 240  
 catacctgcc ggggactggt tgacagcttt aacaaggccc tggagagaac catccggac 300  
 aactttggag gtggaaacac tgccctggag gaagagaatt tgtccaaata caaagacagt 360  
 gagaccgcgc tggtagaggt gctggagggt gtgtgcagca agtcagactt cgagtgcac 420  
 cgccctgctgg agctgagtga ggagctggg gagagctggt ggttcacaa gcagcaggag 480  
 gccccggacc tcttccagtg gctgtgctca gattccctga agtcgtctg ccccgaggc 540  
 acettcgccc cttccctgcct tcctgtcct gggggAACAG agaggccctg cggtgctac 600  
 gggcagtgtg aaggagaagg gacacgaggg ggcagcgggc actgtactg ccaaggccgc 660  
 tacgggggtg aggccctgtgg ccagtgtggc cttggctact ttgaggcaga acgcaacgccc 720  
 agccatctgg tatgttccgc ttgttttggc ccctgtgccc gatgctcagg acctgaggaa 780  
 tcaaactgtt tgcaatgcaa gaagggtctgg gccctgcata acctcaagtgt tgtagacatt 840  
 gatgagtgtg gcacagaggg agccaactgt ggagctgacc aattctgcgt gaacactgag 900  
 ggctccatgt agtgccgaga ctgtgccaag gcctgcctag gtcgcattgg ggcaggggcca 960  
 ggtcgctgtgta agaagtgttag ccctggctat cagcaggtgg gtcgcattgg tctcgatgt 1020  
 gatgagtgtg agacagaggt gtgtccggga gagaacaagc agtgcgtaaaa caccgagggc 1080  
 gtttatcgct gcatctgtgc cgagggtctac aagcagatgg aaggcatctg tgtgaaggag 1140  
 cagatcccaag agtcagcagg cttctctca gagatgacag aagcaggtt ggtggctgt 1200  
 cagcagatgt tccttggcat catcatctgt gcactggcca cgctggctgc taaggcgac 1260  
 ttggtgttca ccgcacatctt cattggggct gtggccggca tgactggcta ctgggtgtca 1320  
 gagcgcagtg accgtgtgt ggagggtctt atcaaggcca gataatcgcc gccaccac 1380  
 gtaggacccctt ctcccaccca cgctgcccc agagcttggg ctgcccctct gctggacact 1440  
 caggacagct tggtttattt ttgagagtgg ggttaagcacc cttacctgcc ttacagagca 1500  
 gcccaggta ccaggcccc ggagacaagg cccctgggtt aaaaagtagc cctgaagggtg 1560  
 gataccatga gcttcacc tggcgcccc acggcaggctt cacaatgtt gaattcaaa 1620  
 agttttccct taatggtggc tgctagact ttggccctgt cttaggatta ggtggcttc 1680  
 acaggggtgg ggccatcaca gtccttcctt gccagctgca tgctgccaat tcctgttctg 1740  
 tgttcaccac atccccacac cccattgcca cttattttt catctcagga aataaagaaa 1800  
 ggtcttggaa agttaaaaaaa aaaaaaaaaa aaaaaaaaaa 1838

<210> 109

<211> 420

<212> PRT

<213> Homo sapiens

<400> 109	Met Ala Pro Trp Pro Pro Lys Gly Leu Val Pro Ala Val Leu Trp Gly
	1 5 10 15
	Leu Ser Leu Phe Leu Asn Leu Pro Gly Pro Ile Trp Leu Gln Pro Ser
	20 25 30
	Pro Pro Pro Gln Ser Ser Pro Pro Pro Gln Pro His Pro Cys His Thr
	35 40 45
	Cys Arg Gly Leu Val Asp Ser Phe Asn Lys Gly Leu Glu Arg Thr Ile
	50 55 60

Arg Asp Asn Phe Gly Gly Asn Thr Ala Trp Glu Glu Glu Asn Leu  
 65 70 75 80

Ser Lys Tyr Lys Asp Ser Glu Thr Arg Leu Val Glu Val Leu Glu Gly  
 85 90 95

Val Cys Ser Lys Ser Asp Phe Glu Cys His Arg Leu Leu Glu Leu Ser  
 100 105 110

Glu Glu Leu Val Glu Ser Trp Trp Phe His Lys Gln Gln Glu Ala Pro  
 115 120 125

Asp Leu Phe Gln Trp Leu Cys Ser Asp Ser Leu Lys Leu Cys Cys Pro  
 130 135 140

Ala Gly Thr Phe Gly Pro Ser Cys Leu Pro Cys Pro Gly Gly Thr Glu  
 145 150 155 160

Arg Pro Cys Gly Gly Tyr Gly Gln Cys Glu Gly Glu Gly Thr Arg Gly  
 165 170 175

Gly Ser Gly His Cys Asp Cys Gln Ala Gly Tyr Gly Gly Glu Ala Cys  
 180 185 190

Gly Gln Cys Gly Leu Gly Tyr Phe Glu Ala Glu Arg Asn Ala Ser His  
 195 200 205

Leu Val Cys Ser Ala Cys Phe Gly Pro Cys Ala Arg Cys Ser Gly Pro  
 210 215 220

Glu Glu Ser Asn Cys Leu Gln Cys Lys Lys Gly Trp Ala Leu His His  
 225 230 235 240

Leu Lys Cys Val Asp Ile Asp Glu Cys Gly Thr Glu Gly Ala Asn Cys  
 245 250 255

Gly Ala Asp Gln Phe Cys Val Asn Thr Glu Gly Ser Tyr Glu Cys Arg  
 260 265 270

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Asp Cys Ala Lys Ala Cys Leu Gly Cys Met Gly Ala Gly Pro Gly Arg  
 275 280 285

Cys Lys Lys Cys Ser Pro Gly Tyr Gln Gln Val Gly Ser Lys Cys Leu  
 290 295 300

Asp Val Asp Glu Cys Glu Thr Glu Val Cys Pro Gly Glu Asn Lys Gln  
 305 310 315 320

Cys Glu Asn Thr Glu Gly Gly Tyr Arg Cys Ile Cys Ala Glu Gly Tyr  
 325 330 335

Lys Gln Met Glu Gly Ile Cys Val Lys Glu Gln Ile Pro Glu Ser Ala  
 340 345 350

Gly Phe Phe Ser Glu Met Thr Glu Asp Glu Leu Val Val Leu Gln Gln  
 355 360 365

Met Phe Phe Gly Ile Ile Ile Cys Ala Leu Ala Thr Leu Ala Ala Lys  
 370 375 380

Gly Asp Leu Val Phe Thr Ala Ile Phe Ile Gly Ala Val Ala Ala Met  
 385 390 395 400

Thr Gly Tyr Trp Leu Ser Glu Arg Ser Asp Arg Val Leu Glu Gly Phe  
 405 410 415

Ile Lys Gly Arg  
 420

<210> 110

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 110

cctggctatc agcaggtggg ctccaaagtgt ctcgatgtgg atgagtgtga

50

<210> 111

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 111

attctgcgtg aacactgagg gc

22

<210> 112

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 112

atctgcttgt agccctcgac ac

22

<210> 113

<211> 1616  
<212> DNA  
<213> Homo sapiens

<220>  
<221> modified\_base  
<222> (1461)  
<223> a, t, c or g

<400> 113  
tgagaccctc ctgcaggcctt ctcaggac agccccactc tgcctttgc tcctccaggg 60  
cagcaccatg cagccccgtt ggctctgt ggcactctgg gtgttgcggc tggccagccc 120  
cgggggccgcc ctgaccgggg agcagctctt gggcagcctg ctgcggcagc tgca gcttcaa 180  
agaggtgcgg accctggaca gggccgacat ggaggagctg gtcattttca cccacgttag 240  
ggcccagtac gtggccctgc tgcagcgcag ccacggggac cgctcccgcg gaaagagggtt 300  
cagccagagc ttccgagagg tgccggcag gttccctggcg ttggaggcca gcacacacct 360  
gctgtgttcc ggcattggagc agcggctgccc gcccacacagc gagctggtgc aggccgtgct 420  
gcggctttc caggagccgg tccccaaaggc cgcgcgtgcac aggccacgggc ggctgtcccc 480  
gcgcagcggcc cggggccggg tgaccgtcga gtggctgcgc gtccgcgcac acggctccaa 540  
ccgcacccctcc ctcatcgact ccaggctgtt gtccgtccac gagagcggct ggaaggccctt 600  
cgacgtgacc gaggccgtga acttctggca gcagctgagc cggccccggc agccgctgtct 660  
gctacaggtg tcgggtcaga gggagcatct gggcccgctg gcttccggcg cccacaagct 720  
ggtcgcgttt gcctcgcagg gggcgcgcagc cgggcttggg gagccccagc tggagctgca 780  
caccctggac ctggggact atggagctca gggcactgt gaccctgaag cacaatgac 840  
cgagggcacc cgctgtgccc gcaggagat gtacattgac ctgcaggaga tgaagtggc 900  
cgagaactgg gtgctggagc ccccgccctt cctggcttat gatgtgtgg gcacccgtgg 960  
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ctcggagact gactcgctgc ccatgatcgat cagcatcaag gagggaggca ggaccaggcc 1080  
ccaggtggtc agectggcca acatgagggt gcagaagtgc agtgtgtcct cggatggtgc 1140  
gctcggtcga aggaggctcc agccataggc gccttagtta gccatcgagg gacttgactt 1200  
gtgtgtgttt ctgaagtgtt cgagggtacc aggagagctg gctgtactg aactgtgtat 1260  
ggacaaaatgc tctgtgtct ctgtgagcc ctgaatttgc ttccctgtac aagttaacctc 1320  
acctaatttt tgcttcctcag gaatgagaat ctttggccac tggagagccc ttgctcagtt 1380  
ttctctattc ttattattca ctgcactata ttctaaagcac ttacatgtgg agataactgta 1440  
acctgaggggc agaaaagccca ntgtgtcatt gtttacttgt cctgtcactg gatctgggct 1500  
aaagtccctcc accaccactc tggacctaag acctggggtt aagtgtgggt tgtcatccc 1560  
caatccagat aataaaagact ttgtaaaaca tgaataaaac acattttattt ctaaaa 1616

<210> 114  
<211> 366  
<212> PRT  
<213> Homo sapiens

<400> 114  
Met Gln Pro Leu Trp Leu Cys Trp Ala Leu Trp Val Leu Pro Leu Ala  
1 5 10 15

Ser Pro Gly Ala Ala Leu Thr Gly Glu Gln Leu Leu Gly Ser Leu Leu  
20 25 30

Arg Gln Leu Gln Leu Lys Glu Val Pro Thr Leu Asp Arg Ala Asp Met  
35 40 45

Glu	Glu	Leu	Val	Ile	Pro	Thr	His	Val	Arg	Ala	Gln	Tyr	Val	Ala	Leu
50								55						60	
Leu	Gln	Arg	Ser	His	Gly	Asp	Arg	Ser	Arg	Gly	Lys	Arg	Phe	Ser	Gln
65						70				75				80	
Ser	Phe	Arg	Glu	Val	Ala	Gly	Arg	Phe	Leu	Ala	Leu	Glu	Ala	Ser	Thr
	85							90					95		
His	Leu	Leu	Val	Phe	Gly	Met	Glu	Gln	Arg	Leu	Pro	Pro	Asn	Ser	Glu
	100						105					110			
Leu	Val	Gln	Ala	Val	Leu	Arg	Leu	Phe	Gln	Glu	Pro	Val	Pro	Lys	Ala
	115						120					125			
Ala	Leu	His	Arg	His	Gly	Arg	Leu	Ser	Pro	Arg	Ser	Ala	Arg	Ala	Arg
	130					135					140				
Val	Thr	Val	Glu	Trp	Leu	Arg	Val	Arg	Asp	Asp	Gly	Ser	Asn	Arg	Thr
	145					150				155			160		
Ser	Leu	Ile	Asp	Ser	Arg	Leu	Val	Ser	Val	His	Glu	Ser	Gly	Trp	Lys
	165						170					175			
Ala	Phe	Asp	Val	Thr	Glu	Ala	Val	Asn	Phe	Trp	Gln	Gln	Leu	Ser	Arg
	180						185					190			
Pro	Arg	Gln	Pro	Leu	Leu	Leu	Gln	Val	Ser	Val	Gln	Arg	Glu	His	Leu
	195						200					205			
Gly	Pro	Leu	Ala	Ser	Gly	Ala	His	Lys	Leu	Val	Arg	Phe	Ala	Ser	Gln
	210						215				220				
Gly	Ala	Pro	Ala	Gly	Leu	Gly	Glu	Pro	Gln	Leu	Glu	Leu	His	Thr	Leu
	225					230				235			240		
Asp	Leu	Gly	Asp	Tyr	Gly	Ala	Gln	Gly	Asp	Cys	Asp	Pro	Glu	Ala	Pro
	245						250					255			
Met	Thr	Glu	Gly	Thr	Arg	Cys	Cys	Arg	Gln	Glu	Met	Tyr	Ile	Asp	Leu
	260						265					270			
Gln	Gly	Met	Lys	Trp	Ala	Glu	Asn	Trp	Val	Leu	Glu	Pro	Pro	Gly	Phe
	275						280					285			
Leu	Ala	Tyr	Glu	Cys	Val	Gly	Thr	Cys	Arg	Gln	Pro	Pro	Glu	Ala	Leu
	290						295					300			
Ala	Phe	Lys	Trp	Pro	Phe	Leu	Gly	Pro	Arg	Gln	Cys	Ile	Ala	Ser	Glu
	305						310				315		320		
Thr	Asp	Ser	Leu	Pro	Met	Ile	Val	Ser	Ile	Lys	Glu	Gly	Gly	Arg	Thr
	325						330					335			

Arg Pro Gln Val Val Ser Leu Pro Asn Met Arg Val Gln Lys Cys Ser  
 340 345 350

Cys Ala Ser Asp Gly Ala Leu Val Pro Arg Arg Leu Gln Pro  
 355 360 365

<210> 115  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 115  
 aggactgcca taacttgcct g 21

<210> 116  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 116  
 ataggagttg aagcagcgct gc 22

<210> 117  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 117  
 tgtgtggaca tagacgagtg ccgctaccgc tactgccagc accgc 45

<210> 118  
<211> 1857  
<212> DNA  
<213> Homo sapiens

<400> 118  
 gtctgttccc aggagtccctt cggcggtgtgt tgtgtcagtgcgcctgatgcgatggggaca 60  
 aaggcgcaag tcgagaggaa actgttgtgc ctcttcataat tggcgatcct gttgtgctcc 120  
 ctggcattgg gcagtgttac agtgcactct tctgaacctg aagtcaaat tcctgagaat 180

aatcctgtga agttgtcctg tgccctactcg ggctttctt ctccccgtgt ggagtggaaag 240  
 tttgaccaag gagacaccac cagactcggt tgctataata acaagatcac agcttcstat 300  
 gaggaccggg tgaccttctt gccaactgggt atcacctca agtccgtgac acggaaagac 360  
 actgggacat acacttgtat ggtctctgag gaaggcggca acagctatgg ggaggtcaag 420  
 gtcaagctca tcgtgcttgc gcctccatcc aagcctacag ttaacatccc ctcctctgcc 480  
 accattggga accgggcagt gctgacatgc tcagaacaag atggttcccc accttctqaa 540  
 tacacctggc tcaaagatgg gatagtgtat cctacgaatc cccaaaagcac ccgtgccttc 600  
 agcaactctt cctatgtcctt gaatcccaca acaggagagc tggctttga tccctgtca 660  
 gcctctgata ctggagaata cagctgtgag gcacggaaatg ggtatgggac acccatgact 720  
 tcaaatgtcg tgccatggc agctgtggag cggaatgtgg gggtcatcg ggcagccgtc 780  
 cttgtAACCC tgatttcctt gggaaatctt gttttggca tctggtttc ctataggcga 840  
 ggcactttg acagaacaaa gaaagggact tcgagtaaga aggtgattta cagccagcct 900  
 agtgcggaa gtgaaggaga attcaaacag acctcgatcat tcctgggtgtg agcctggcgt 960  
 gctcaccggc tatcatctgc atttgcctt ctcagtgct accggactct ggccctgtat 1020  
 gtctgttagtt tcacaggatg ctttattttgt cttctacacc ccacaggggcc ccctacttct 1080  
 tcggatgtgt tttaataat gtcagctatg tgcccatcc tccttcatgc cctccctccc 1140  
 ttccctacca ctgctgagtg gcctggaaact tgtttaaagt gtttattccc cattttttg 1200  
 agggatcagg aaggaatctt gggatgcca ttgacttccc ttctaagttag acagaaaaaa 1260  
 tggcgggggt cgcaggaatc tgccactcaac tgcccacctg gctggcaggg atctttgaat 1320  
 aggtatctt agcttggttc tgggctctt ctttgcgtac tgacgaccag ggccagctgt 1380  
 tctagagcgg gaatttagagg cttagagcggc tgaaatgggtt gtttggtgat gacactgggg 1440  
 tccttcatc tctggggccc actctttctt gtcttccat gggaaatgtcc actgggatcc 1500  
 ctctgcctg tcctcctgaa tacaagctga ctgacattga ctgtgtctgt ggaaatggg 1560  
 agctcttgcgtt gtggagagca tagtaaattt tcagagaact tgaagccaaa aggatttaaa 1620  
 accgctgctc taaagaaaaag aaaactggag gctggcgca gtggctcagc cctgtaatcc 1680  
 cagaggctga ggcaggcggc tcacctgagg tcgggagttc gggatcagcc tgaccaacat 1740  
 ggagaaaaccc tactggaaat acaaagttt ccaggcatgg tggtgcatgc ctgtagtc 1800  
 agctgctcag gacccctggc acaagagcaa aactccagct caaaaaaaaaa aaaaaaaaaa 1857

<210> 119  
 <211> 299  
 <212> PRT  
 <213> Homo sapiens

<400> 119  
 Met Gly Thr Lys Ala Gln Val Glu Arg Lys Leu Leu Cys Leu Phe Ile  
 1 5 10 15

Leu Ala Ile Leu Leu Cys Ser Leu Ala Leu Gly Ser Val Thr Val His  
 20 25 30

Ser Ser Glu Pro Glu Val Arg Ile Pro Glu Asn Asn Pro Val Lys Leu  
 35 40 45

Ser Cys Ala Tyr Ser Gly Phe Ser Ser Pro Arg Val Glu Trp Lys Phe  
 50 55 60

Asp Gln Gly Asp Thr Thr Arg Leu Val Cys Tyr Asn Asn Lys Ile Thr  
 65 70 75 80

Ala Ser Tyr Glu Asp Arg Val Thr Phe Leu Pro Thr Gly Ile Thr Phe  
 85 90 95

Lys Ser Val Thr Arg Glu Asp Thr Gly Thr Tyr Thr Cys Met Val Ser  
 100 105 110  
 Glu Glu Gly Gly Asn Ser Tyr Gly Glu Val Lys Val Lys Leu Ile Val  
 115 120 125  
 Leu Val Pro Pro Ser Lys Pro Thr Val Asn Ile Pro Ser Ser Ala Thr  
 130 135 140  
 Ile Gly Asn Arg Ala Val Leu Thr Cys Ser Glu Gln Asp Gly Ser Pro  
 145 150 155 160  
 Pro Ser Glu Tyr Thr Trp Phe Lys Asp Gly Ile Val Met Pro Thr Asn  
 165 170 175  
 Pro Lys Ser Thr Arg Ala Phe Ser Asn Ser Ser Tyr Val Leu Asn Pro  
 180 185 190  
 Thr Thr Gly Glu Leu Val Phe Asp Pro Leu Ser Ala Ser Asp Thr Gly  
 195 200 205  
 Glu Tyr Ser Cys Glu Ala Arg Asn Gly Tyr Gly Thr Pro Met Thr Ser  
 210 215 220  
 Asn Ala Val Arg Met Glu Ala Val Glu Arg Asn Val Gly Val Ile Val  
 225 230 235 240  
 Ala Ala Val Leu Val Thr Leu Ile Leu Gly Ile Leu Val Phe Gly  
 245 250 255  
 Ile Trp Phe Ala Tyr Ser Arg Gly His Phe Asp Arg Thr Lys Lys Gly  
 260 265 270  
 Thr Ser Ser Lys Lys Val Ile Tyr Ser Gln Pro Ser Ala Arg Ser Glu  
 275 280 285  
 Gly Glu Phe Lys Gln Thr Ser Ser Phe Leu Val  
 290 295  
 <210> 120  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
       oligonucleotide probe  
 <400> 120  
 tcgcggagct gtgttctgtt tccc  
 <210> 121  
 <211> 50

<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 121  
tgatcgcgat ggggacaaag gcgcaggctc gagaggaaac tttgtgcct 50

<210> 122  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 122  
acacctgggtt caaagatggg 20

<210> 123  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 123  
taggaagagt tgctgaaggc acgg 24

<210> 124  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 124  
ttgccttact caggtgctac 20

<210> 125  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic

## oligonucleotide probe

<400> 125  
actcagcagt ggttagaaag 20

<210> 126  
<211> 1210  
<212> DNA  
<213> Homo sapiens

<400> 126  
cagcgcgtgg cggcgccgc tgggggaca gcatgagcgg cggttggatg ggcgcagg 60  
gagcgtggcg aacaggggct ctgggcctgg cgctgctgct gctgctcgcc ctcgactag 120  
gcctggaggc cggcgccgc cccgtttcca ccccgaccc tcggccaggcc gcaggcccc 180  
gctcaggctc gtggccaccc accaagttcc agtgcgcac cagtggctta tgcgtgcccc 240  
tcacctggcg ctgcgacagg gacttggact gcagcgatgg cagcgatgag gaggagtgc 300  
ggattgagcc atgtaccagg aaagggaat gcccacccgc ccctggccctc ccctgcccc 360  
gcacccggcgt cagtgactgc tctggggaa ctgacaagaa actgcgcac tgcagccgc 420  
tggcctgcct agcaggcgag ctccgttgca cgctgagcga tgactgcatt ccactcacgt 480  
ggcgcgtgcga cggccacccca gactgtcccg actccagcga cgagctcgcc tgtgaacca 540  
atgagatcct cccggaaggg gatgccacaa ccatggggcc ccctgtgacc ctggagagt 600  
tcacctctct caggaatgcc acaaccatgg ggccccctgt gaccctggag agtgcctcc 660  
ctgtcgggaa tgccacatcc tcctctgccc gagaccagtc tggaaagccca actgcctatg 720  
gggttattgc agctgtgcg gtgctcagtg caagcctggt caccgcacc ctcctccctt 780  
tgcctggct ccgagcccg gagcgcctcc gcccactggg gttactggg gccatgaagg 840  
agtccctgct gctgtcagaa cagaagacot cgctgcctg aggacaagca cttggccacca 900  
ccgtcactca gcccctggcg tagccggaca ggaggagagc agtgtatggc atgggtaccc 960  
gggcacacca gcccctcagag acctgagttc ttctggccac gtggaaacctc gaacccgagc 1020  
tcctgcagaa gtggccctgg agattgaggg tccctggaca ctccctatgg agatccgggg 1080  
agctaggatg gggaaacctgc cacagccaga actgaggggc tggcccccagg cagctcccag 1140  
gggtagaaac gcccctgtgc ttaagacact ccctgtgcc ccgtctgagg gtggcgatta 1200  
aagttgcctc 1210

<210> 127  
<211> 282  
<212> PRT  
<213> Homo sapiens

<400> 127  
Met Ser Gly Gly Trp Met Ala Gln Val Gly Ala Trp Arg Thr Gly Ala  
1 5 10 15

Leu Gly Leu Ala Leu Leu Leu Leu Gly Leu Gly Leu Gly Leu Glu  
20 25 30

Ala Ala Ala Ser Pro Leu Ser Thr Pro Thr Ser Ala Gln Ala Ala Gly  
35 40 45

Pro Ser Ser Gly Ser Cys Pro Pro Thr Lys Phe Gln Cys Arg Thr Ser  
50 55 60

Gly Leu Cys Val Pro Leu Thr Trp Arg Cys Asp Arg Asp Leu Asp Cys  
65 70 75 80

Ser Asp Gly Ser Asp Glu Glu Glu Cys Arg Ile Glu Pro Cys Thr Gln  
                   85                         90                         95  
  
 Lys Gly Gln Cys Pro Pro Pro Pro Gly Leu Pro Cys Pro Cys Thr Gly  
                   100                     105                         110  
  
 Val Ser Asp Cys Ser Gly Gly Thr Asp Lys Lys Leu Arg Asn Cys Ser  
                   115                     120                         125  
  
 Arg Leu Ala Cys Leu Ala Gly Glu Leu Arg Cys Thr Leu Ser Asp Asp  
                   130                     135                         140  
  
 Cys Ile Pro Leu Thr Trp Arg Cys Asp Gly His Pro Asp Cys Pro Asp  
                   145                     150                     155                 160  
  
 Ser Ser Asp Glu Leu Gly Cys Gly Thr Asn Glu Ile Leu Pro Glu Gly  
                   165                     170                         175  
  
 Asp Ala Thr Thr Met Gly Pro Pro Val Thr Leu Glu Ser Val Thr Ser  
                   180                     185                         190  
  
 Leu Arg Asn Ala Thr Thr Met Gly Pro Pro Val Thr Leu Glu Ser Val  
                   195                     200                         205  
  
 Pro Ser Val Gly Asn Ala Thr Ser Ser Ser Ala Gly Asp Gln Ser Gly  
                   210                     215                         220  
  
 Ser Pro Thr Ala Tyr Gly Val Ile Ala Ala Ala Val Leu Ser Ala  
                   225                     230                         235                 240  
  
 Ser Leu Val Thr Ala Thr Leu Leu Leu Ser Trp Leu Arg Ala Gln  
                   245                     250                         255  
  
 Glu Arg Leu Arg Pro Leu Gly Leu Leu Val Ala Met Lys Glu Ser Leu  
                   260                     265                         270  
  
 Leu Leu Ser Glu Gln Lys Thr Ser Leu Pro  
                   275                     280  
  
 <210> 128  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
           oligonucleotide probe  
  
 <400> 128  
 aagttccagt gccgcaccag tggc  
  
 <210> 129

<211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 129  
 ttgttccac agccgagctc gtcg 24

<210> 130  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 130  
 gaggaggagt gcaggattga gccatgtacc cagaaaggc aatgccacc 50

<210> 131  
 <211> 1843  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> modified\_base  
 <222> (1837)  
 <223> a, t, c or g

<400> 131  
 cccacgcgtc cggtctcgct cgctcgcgca gcggcgccag cagaggtcgc gcacagatgc 60  
 gggtagact ggcgggggga ggaggcggag gagggaaagga agctgcattgc atgagaccca 120  
 cagactcttg caagctggat gcccctgtg gatgaaaat gtatcatgaa atgaacccga 180  
 gcaatggaga tggatttcta gagcagcagc agcagcagca gcaacctcag tccccccaga 240  
 gactcttggc cgtgatcctg tggtttcage tggcgctgtg ctccggccct gcacagctca 300  
 cggcggggtt cgatgacattt caagtgtgtg ctgaccccg cattcccgag aatgcttca 360  
 ggaccccccag cggagggggtt ttctttgaag gctctgttagc ccgatttac tgccaagacg 420  
 gattcaagct gaagggcgct acaaagagac tgggtttgaa gcattttaat ggaaccttag 480  
 gctggatccc aagtgataat tccatctgtg tgcaagaaga ttgcccgtatc cctcaaatcg 540  
 aagatgctga gattcataac aagacatata gacatggaga gaaqctaatac atcaattgtc 600  
 atgaaggatt caagatccgg taccccgacc tacacaatat ggtttcatta tgtcgcgatg 660  
 atggaacgtg gaataatctg cccatctgtc aaggctgcct gagacctcta gcctcttcta 720  
 atggctatgt aaacatctt gagctccaga cctccctccc ggtggggact gtgatctct 780  
 atcgctgctt tccccggattt aaacttgatg ggtctcgta ttttgatgtc ttacaaaacc 840  
 ttatctggtc gtccagccca ccccggtgcc ttgctctgga agcccaagtc tgtccactac 900  
 ctccaaatggt gagtcacgga gatttcgtct gcccacccgc gccttgcgag cgctacaacc 960  
 acggaactgt ggtggagtt tactgcgtc ctggctacag cctcaccaggc gactacaagt 1020  
 acatcacctg ccagtatgga gagtggtttc cttcttatca agtctactgc atcaaatcag 1080  
 agccaaacgtg gcccagcacc catgagaccc tcctgaccac gtggaaaggatt gtggcggtca 1140

cgccaaccag tgtgctgctg gtgctgctgc tcgtcatcct ggccaggatg ttccagacca 1200  
 agttcaaggc ccacttccc cccagggggc ctccccggag ttccagcagt gaccctgact 1260  
 ttgtggtgtt agacggcggt cccgtcatgc tcccgtccta tgacgaagct gtgagtggcg 1320  
 gcttgagtgc cttaggcccc gggtacatgg cctctgtggg ccagggctgc cccttacccg 1380  
 tggacgacca gagccccca gcatacccg gtcagggga cacggacaca ggcccagggg 1440  
 agtcagaaac ctgtgacagc gtctcagget cttctgagct gtcacaaagt ctgtattcac 1500  
 ctccccagggtg ccaagagagc acccaccctg ctccggacaa ccctgacata attgccagca 1560  
 cgccagagga ggtggcatcc accagcccg gcatccatca tgcccactgg gtgttgttcc 1620  
 taagaaaactg attgattaaa aaatttccca aagtgcctg aagtgtctct tcaaatacat 1680  
 gttgatctgt ggagttgatt ccttccttc tcttggtttt agacaaatgt aaacaaagct 1740  
 ctgatcctta aaattgctat gctgatagag tggtagggc tggaaagcttg atcaagtcct 1800  
 gtttcttctt gacacagact gattaaaaat taaaagnaaa aaa 1843

<210> 132

<211> 490

<212> PRT

<213> Homo sapiens

<400> 132

Met	Tyr	His	Gly	Met	Asn	Pro	Ser	Asn	Gly	Asp	Gly	Phe	Leu	Glu	Gln
1					5									10	15

Gln	Gln	Gln	Gln	Gln	Pro	Gln	Ser	Pro	Gln	Arg	Leu	Leu	Ala	Val
20						25							30	

Ile	Leu	Trp	Phe	Gln	Leu	Ala	Leu	Cys	Phe	Gly	Pro	Ala	Gln	Leu	Thr
35						40						45			

Gly	Gly	Phe	Asp	Asp	Leu	Gln	Val	Cys	Ala	Asp	Pro	Gly	Ile	Pro	Glu
50					55						60				

Asn	Gly	Phe	Arg	Thr	Pro	Ser	Gly	Gly	Val	Phe	Phe	Glu	Gly	Ser	Val
65					70					75			80		

Ala	Arg	Phe	His	Cys	Gln	Asp	Gly	Phe	Lys	Leu	Lys	Gly	Ala	Thr	Lys
85						90						95			

Arg	Leu	Cys	Leu	Lys	His	Phe	Asn	Gly	Thr	Leu	Gly	Trp	Ile	Pro	Ser
100						105					110				

Asp	Asn	Ser	Ile	Cys	Val	Gln	Glu	Asp	Cys	Arg	Ile	Pro	Gln	Ile	Glu
115						120					125				

Asp	Ala	Glu	Ile	His	Asn	Lys	Thr	Tyr	Arg	His	Gly	Glu	Lys	Leu	Ile
130						135					140				

Ile	Thr	Cys	His	Glu	Gly	Phe	Lys	Ile	Arg	Tyr	Pro	Asp	Leu	His	Asn
145						150					155			160	

Met	Val	Ser	Leu	Cys	Arg	Asp	Asp	Gly	Thr	Trp	Asn	Asn	Leu	Pro	Ile
165						170					175				

Cys Gln Gly Cys Leu Arg Pro Leu Ala Ser Ser Asn Gly Tyr Val Asn

180	185	190
Ile Ser Glu Leu Gln Thr Ser Phe Pro Val Gly Thr Val Ile Ser Tyr		
195	200	205
Arg Cys Phe Pro Gly Phe Lys Leu Asp Gly Ser Ala Tyr Leu Glu Cys		
210	215	220
Leu Gln Asn Leu Ile Trp Ser Ser Ser Pro Pro Arg Cys Leu Ala Leu		
225	230	235
Glu Ala Gln Val Cys Pro Leu Pro Pro Met Val Ser His Gly Asp Phe		
245	250	255
Val Cys His Pro Arg Pro Cys Glu Arg Tyr Asn His Gly Thr Val Val		
260	265	270
Glu Phe Tyr Cys Asp Pro Gly Tyr Ser Leu Thr Ser Asp Tyr Lys Tyr		
275	280	285
Ile Thr Cys Gln Tyr Gly Glu Trp Phe Pro Ser Tyr Gln Val Tyr Cys		
290	295	300
Ile Lys Ser Glu Gln Thr Trp Pro Ser Thr His Glu Thr Leu Leu Thr		
305	310	315
Thr Trp Lys Ile Val Ala Phe Thr Ala Thr Ser Val Leu Leu Val Leu		
325	330	335
Leu Leu Val Ile Leu Ala Arg Met Phe Gln Thr Lys Phe Lys Ala His		
340	345	350
Phe Pro Pro Arg Gly Pro Pro Arg Ser Ser Ser Ser Asp Pro Asp Phe		
355	360	365
Val Val Val Asp Gly Val Pro Val Met Leu Pro Ser Tyr Asp Glu Ala		
370	375	380
Val Ser Gly Gly Leu Ser Ala Leu Gly Pro Gly Tyr Met Ala Ser Val		
385	390	395
Gly Gln Gly Cys Pro Leu Pro Val Asp Asp Gln Ser Pro Pro Ala Tyr		
405	410	415
Pro Gly Ser Gly Asp Thr Asp Thr Gly Pro Gly Glu Ser Glu Thr Cys		
420	425	430
Asp Ser Val Ser Gly Ser Ser Glu Leu Leu Gln Ser Leu Tyr Ser Pro		
435	440	445
Pro Arg Cys Gln Glu Ser Thr His Pro Ala Ser Asp Asn Pro Asp Ile		
450	455	460

Ile Ala Ser Thr Ala Glu Glu Val Ala Ser Thr Ser Pro Gly Ile His  
 465 470 475 480

His Ala His Trp Val Leu Phe Leu Arg Asn  
 485 490

<210> 133

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 133

atctcctatac gctgcttcc cggt

23

<210> 134

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 134

agccaggatc gcagtaaaaac tcc

23

<210> 135

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 135

atttaaactt gatgggtctg cgtatcttga gtgcttacaa aacccttatct

50

<210> 136

<211> 1815

<212> DNA

<213> Homo sapiens

<400> 136

ccccacgcgtc cgctccgcgc cctccccccc gcctcccggt cggtccgtcg gtggcctaga 60  
 gatgtctgtc ccgcgggtgc agttgtcgcg cacgcctctg cccgcgcagcc cgctccaccc 120  
 ccgttagcgcc cgagtgtcgg ggggcgcacc cgagtgggc catgaggccg ggaaccgcgc 180  
 tacaggccgt gctgtggcc gtgtgtgtgg tggggctgcg ggccgcgacg ggtcgccctgc 240  
 tgagtgcctc ggatttggac ctcagaggag ggcagccagt ctgccgggaa gggacacaga 300

ggccttgtta	taaagtcat	tactccatg	atacttctcg	aagactgaac	tttgaggaag	360
ccaaagaagc	ctgcaggagg	gatggaggcc	agctagtca	catcgagtct	gaagatgaac	420
agaaaactgt	agaaaaagttc	attgaaaacc	tcttgccatc	tgatgggtac	ttctggattg	480
ggctcaggag	gcgtgaggag	aaacaaagca	atagcacagc	ctgcaggac	ctttatgtt	540
ggactgatgg	cagcatatca	caatttagga	actggatgt	ggatgagccg	tcctgcggca	600
gcgaggctg	cgtggatcatg	taccatcagc	catccggacc	cgctggatc	ggaggcccct	660
acatgttcca	gtggaatgtat	gaccgttgca	acatgaagaa	caatttcatt	tgcaaataatt	720
ctgatgagaa	accagcagtt	ccttcttagag	aagctgaagg	tgaggaaaca	gagctgacaa	780
cacctgtact	tccagaagaa	acacaggaag	aagatgccaa	aaaaacattt	aaagaaaagta	840
gagaagctgc	cttgaatctg	gcctacatcc	taatccccag	cattccctt	ctccctccct	900
ttgtggtcac	cacagttgtt	tgttgggtt	ggatctgtag	aaaaagaaaa	cgggagcagc	960
cagaccctag	cacaaagaag	caacacacca	tctggccctc	tcctcaccag	ggaaacagcc	1020
cgAACCTAGA	GGTCTACAA	GTCATAAGAA	AACAAAGCGA	AGCTGACTTA	GCTGAGACCC	1080
ggccagacct	gaagaatatt	tcattccgag	tgtgttcggg	agaagccact	cccgatgaca	1140
tgtcttgtga	ctatgacaac	atggctgtga	accatcaga	aagtgggtt	gtgactctgg	1200
tgagcgtgga	gagtggattt	gtgaccaatg	acatttatga	gttctccca	gaccaaattgg	1260
ggaggagtaa	ggagtctgga	tgggtggaaa	atgaaatata	tggttattag	gacatataaa	1320
aaactgaaac	tgacaacaat	ggaaaagaaa	tgataagcaa	aatcctctta	ttttctataa	1380
ggaaaataca	cagaaggct	atgaacaagc	ttagatcagg	tcctgtggat	gagcatgtgg	1440
tccccacgac	ctccctgttgg	accccccacgt	tttggctgt	tcctttatcc	cagccagtca	1500
tccagctcga	ccttatgaga	aggtacccctg	cccaggtctg	gcacatagta	gagtctcaat	1560
aaatgtca	tgttgggtt	tatctaactt	ttaagggaca	gagctttacc	ttggcagtgtat	1620
aaagatgggc	tgtggagctt	ggaaaaccac	ctctgttttc	cttgctctat	acagcagcac	1680
atattatcat	acagacagaa	aatcoagaat	cttttcaaag	cccacatag	gtagcacagg	1740
ttggccctgt	catcggcaat	tctcatatct	gttttttca	aagaataaaaa	tcaaataaaag	1800
accaqqaaaa	aaaaaa					1815

<210> 137

<211> 382

<212> PRT

<213> Homo sapiens

<400> 137

Met Arg P

1                    5                    10                    15

Val Gly Leu Arg Ala Ala Thr Gly Arg Leu Leu Ser Ala Ser Asp Leu  
20 25 30

Asp Leu Arg Gly Gly Gln Pro Val Cys Arg Gly Gly Thr Gln Arg Pro  
35 40 45 .

Cys Tyr Lys Val Ile Tyr Phe His Asp Thr Ser Arg Arg Leu Asn Phe  
50 55 60

Ile Glu Ser Glu Asp Glu Gln Lys Leu Ile Glu Lys Phe Ile Glu Asn  
85 90 95

Leu Leu Pro Ser Asp Gly Asp Phe Trp Ile Gly Leu Arg Arg Arg Glu  
                   100                 105                 110

Glu Lys Gln Ser Asn Ser Thr Ala Cys Gln Asp Leu Tyr Ala Trp Thr  
 115 120 125  
 Asp Gly Ser Ile Ser Gln Phe Arg Asn Trp Tyr Val Asp Glu Pro Ser  
 130 135 140  
 Cys Gly Ser Glu Val Cys Val Val Met Tyr His Gln Pro Ser Ala Pro  
 145 150 155 160  
 Ala Gly Ile Gly Gly Pro Tyr Met Phe Gln Trp Asn Asp Asp Arg Cys  
 165 170 175  
 Asn Met Lys Asn Asn Phe Ile Cys Lys Tyr Ser Asp Glu Lys Pro Ala  
 180 185 190  
 Val Pro Ser Arg Glu Ala Glu Gly Glu Glu Thr Glu Leu Thr Thr Pro  
 195 200 205  
 Val Leu Pro Glu Glu Thr Gln Glu Glu Asp Ala Lys Lys Thr Phe Lys  
 210 215 220  
 Glu Ser Arg Glu Ala Ala Leu Asn Leu Ala Tyr Ile Leu Ile Pro Ser  
 225 230 235 240  
 Ile Pro Leu Leu Leu Leu Val Val Thr Thr Val Val Cys Trp Val  
 245 250 255  
 Trp Ile Cys Arg Lys Arg Lys Arg Glu Gln Pro Asp Pro Ser Thr Lys  
 260 265 270  
 Lys Gln His Thr Ile Trp Pro Ser Pro His Gln Gly Asn Ser Pro Asp  
 275 280 285  
 Leu Glu Val Tyr Asn Val Ile Arg Lys Gln Ser Glu Ala Asp Leu Ala  
 290 295 300  
 Glu Thr Arg Pro Asp Leu Lys Asn Ile Ser Phe Arg Val Cys Ser Gly  
 305 310 315 320  
 Glu Ala Thr Pro Asp Asp Met Ser Cys Asp Tyr Asp Asn Met Ala Val  
 325 330 335  
 Asn Pro Ser Glu Ser Gly Phe Val Thr Leu Val Ser Val Glu Ser Gly  
 340 345 350  
 Phe Val Thr Asn Asp Ile Tyr Glu Phe Ser Pro Asp Gln Met Gly Arg  
 355 360 365  
 Ser Lys Glu Ser Gly Trp Val Glu Asn Glu Ile Tyr Gly Tyr  
 370 375 380

<211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 138  
 gttcattgaa aaccttgc catctgatgg tgacttctgg attgggctca 50

<210> 139  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 139  
 aagccaaaga agcctgcagg aggg 24

<210> 140  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 140  
 cagtccaaggataaaagggtcc tggc 24

<210> 141  
 <211> 1514  
 <212> DNA  
 <213> Homo sapiens

<400> 141

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ggggtctccc tcagggccgg gaggcacacgc ggccctgtctgctgaagggtt ctggatgtac 60  
 gcatccgcag gttcccgccgg acttgggggc gcccgcgtgag ccccgccgcgcccc cgcaagaagac 120  
 ttgtgtttgc ctctgcgcgctcaacccgg aggccagcga gggcctacca ccatgatcac 180  
 tggtgtgttc agcatgcgtctgtggacccc agtgggcgtc ctgcacctcgctggcgtaactg 240  
 cctgcaccag cggcggttgg ccctggccga gctgcaggag gccgatggcc agtgtccgg 300  
 cgaccgcagc ctgtgtgaagt tgaaaatgggt gcaggtcggt tttcgacacg gggctcgag 360  
 tcctctcaag ccgctccgc tgaggagaca ggttagagtgg aaccccccagc tattagaggt 420  
 cccaccccaa actcagtttgc attacacagt caccaatcta gctgggtggc cgaaaccata 480  
 ttctccttac gactctaat accatgagac caccctgaag gggggcatgt ttgctggca 540  
 gctgaccaag gtgggcattgc agcaaatgtt tgccttggga gagagactga ggaagaacta 600  
 tgtgaaagac attcccttgc ttccaccaac cttcaacccca caggaggctt ttattcggttc 660  
 cactaacatt tttcgaaatc tggagtccac cgggttttg ctggctggc tttccagtg 720

tcagaaaagaa ggaccatca tcatccacac tcatgaagca gattcagaag tcttgatcc 780  
 caactaccaa agctgctgga gcctgaggca gagaaccaga ggccggaggc agactgcctc 840  
 ttacagcca ggaatctcg aggatttcaa aaaggtgaag gacaggatgg gcattgacag 900  
 tagtgataaa gtggacttct tcatcctcct ggacaacgtg gtcggcggc aggcacacaa 960  
 cctcccaagc tgccccatgc tgaagagatt tgcacggatg atcgaacaga gagctgtgga 1020  
 cacatccttgc tacatactgc ccaaggaaga cagggaaagt cttcagatgg cagtaggccc 1080  
 attcctccac atccttagaga gcaacctgct gaaagccatg gactctgcca ctgccccgaa 1140  
 caagatcaga aagctgtatc tctatgcggc tcatgatgtg accttcatac cgctcttaat 1200  
 gaccctgggg attttggacc acaaattggcc accgtttgc gttgacactga ccatggaact 1260  
 ttaccagcac ctggaatcta aggagtgggt tgcagctc tattaccacg ggaaggagca 1320  
 ggtgccgaga ggttgcctg atgggctctg cccgcggac atgttcttga atgcctatgtc 1380  
 agtttatacc ttaagccag aaaaatacca tgcactctgc tctcaaactc aggtgatgga 1440  
 agtggaaat gaagagtaac tgatttataa aagcaggatg tggatttt aaaataaaagt 1500  
 gccttataac aatg 1514

&lt;210&gt; 142

&lt;211&gt; 428

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 142

Met	Ile	Thr	Gly	Val	Phe	Ser	Met	Arg	Leu	Trp	Thr	Pro	Val	Gly	Val
1							5			10					15

Leu	Thr	Ser	Leu	Ala	Tyr	Cys	Leu	His	Gln	Arg	Arg	Val	Ala	Leu	Ala
							20		25					30	

Glu	Leu	Gln	Glu	Ala	Asp	Gly	Gln	Cys	Pro	Val	Asp	Arg	Ser	Leu	Leu
							35		40				45		

Lys	Leu	Lys	Met	Val	Gln	Val	Val	Phe	Arg	His	Gly	Ala	Arg	Ser	Pro
							50		55			60			

Leu	Lys	Pro	Leu	Pro	Leu	Glu	Glu	Gln	Val	Glu	Trp	Asn	Pro	Gln	Leu
							65		70		75		80		

Leu	Glu	Val	Pro	Pro	Gln	Thr	Gln	Phe	Asp	Tyr	Thr	Val	Thr	Asn	Leu
							85		90				95		

Ala	Gly	Gly	Pro	Lys	Pro	Tyr	Ser	Pro	Tyr	Asp	Ser	Gln	Tyr	His	Glu
							100		105			110			

Thr	Thr	Leu	Lys	Gly	Gly	Met	Phe	Ala	Gly	Gln	Leu	Thr	Lys	Val	Gly
						115		120				125			

Met	Gln	Gln	Met	Phe	Ala	Leu	Gly	Glu	Arg	Leu	Arg	Lys	Asn	Tyr	Val
						130		135			140				

Glu	Asp	Ile	Pro	Phe	Leu	Ser	Pro	Thr	Phe	Asn	Pro	Gln	Glu	Val	Phe
							145		150		155		160		

Ile	Arg	Ser	Thr	Asn	Ile	Phe	Arg	Asn	Leu	Glu	Ser	Thr	Arg	Cys	Leu
							165		170			175			

Leu Ala Gly Leu Phe Gln Cys Gln Lys Glu Gly Pro Ile Ile Ile His  
 180 185 190

Thr Asp Glu Ala Asp Ser Glu Val Leu Tyr Pro Asn Tyr Gln Ser Cys  
 195 200 205

Trp Ser Leu Arg Gln Arg Thr Arg Gly Arg Arg Gln Thr Ala Ser Leu  
 210 215 220

Gln Pro Gly Ile Ser Glu Asp Leu Lys Lys Val Lys Asp Arg Met Gly  
 225 230 235 240

Ile Asp Ser Ser Asp Lys Val Asp Phe Phe Ile Leu Leu Asp Asn Val  
 245 250 255

Ala Ala Glu Gln Ala His Asn Leu Pro Ser Cys Pro Met Leu Lys Arg  
 260 265 270

Phe Ala Arg Met Ile Glu Gln Arg Ala Val Asp Thr Ser Leu Tyr Ile  
 275 280 285

Leu Pro Lys Glu Asp Arg Glu Ser Leu Gln Met Ala Val Gly Pro Phe  
 290 295 300

Leu His Ile Leu Glu Ser Asn Leu Leu Lys Ala Met Asp Ser Ala Thr  
 305 310 315 320

Ala Pro Asp Lys Ile Arg Lys Leu Tyr Leu Tyr Ala Ala His Asp Val  
 325 330 335

Thr Phe Ile Pro Leu Leu Met Thr Leu Gly Ile Phe Asp His Lys Trp  
 340 345 350

Pro Pro Phe Ala Val Asp Leu Thr Met Glu Leu Tyr Gln His Leu Glu  
 355 360 365

Ser Lys Glu Trp Phe Val Gln Leu Tyr Tyr His Gly Lys Glu Gln Val  
 370 375 380

Pro Arg Gly Cys Pro Asp Gly Leu Cys Pro Leu Asp Met Phe Leu Asn  
 385 390 395 400

Ala Met Ser Val Tyr Thr Leu Ser Pro Glu Lys Tyr His Ala Leu Cys  
 405 410 415

Ser Gln Thr Gln Val Met Glu Val Gly Asn Glu Glu  
 420 425

<210> 143  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 143  
ccaactacca aagctgctgg agcc 24

<210> 144  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 144  
gcagctctat taccacggga agga 24

<210> 145  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 145  
tccttcccgt ggtaatagag ctgc 24

<210> 146  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 146  
ggcagagaac cagaggccgg aggagactgc ctcttacag ccagg 45

<210> 147  
<211> 1686  
<212> DNA  
<213> Homo sapiens

<400> 147  
ctcctcttaa catacttgca gctaaaacta aatattgctg cttggggacc tccttcttagc 60  
cttaaaatttc agctcatcac cttcacctgc cttgggtcatg gctctgctat ttccttgat 120  
ccttgccatt tgcaccagac ctggattcct agcgctcaca tctggagtgc ggctgggtggg 180

gggcctccac cgctgtgaag ggccgggtgga ggtggAACAG aaaggccagt ggggcaccgt 240  
 gtgtgatgac ggctgggaca ttaaggacgt ggctgtgtt tgccgggagc tggctgtgg 300  
 agctgccagc ggaaccccta gtggatttt gtatgagcca ccagcagaaa aagagcaaaa 360  
 ggtcctcatc caatcagtca gttgcacagg aacagaagat acattggctc agtgtgagca 420  
 agaagaagtt tatgattgtt cacatgtatc agatgtggg gcatcggtg agaaccaga 480  
 gagcttttc tccccagtcc cagagggtgt caggctggct gacggccctg ggcattgcaa 540  
 gggacgcgtg gaagtgaagc accagaacca gtggatacc gtgtccaga caggctggag 600  
 cctccgggccc gcaaagggtgg tgtgcggca gctggatgt gggagggctg tactgactca 660  
 aaaacgctgc aacaagcatg cctatggccg aaaacccatc tggctgagcc agatgtcatg 720  
 ctcaggacga gaagcaaccc ttcaggattt ccctctggg cttggggga agaacaccc 780  
 caaccatgat gaagacacgt gggtcgaatg tgaagatccc tttgacttga gacttaggg 840  
 aggagacaac ctctgtctg ggcgacttga ggtgtgcac aaggggctat gggctctgt 900  
 ctgtgatgac aactggggag aaaaggagga ccaggtggta tgcaagcaac tggctgtgg 960  
 gaagtccctc ttccttcct tcagagaccc gaaatgttat ggcctgggg ttggccgcat 1020  
 ctggctggat aatgttcgtt gtcaggggg ggagcagtcc ctggagcagt gccagcacag 1080  
 attttggggg tttcactgact gcacccacca ggaagatgtg gctgtcatct gctcagtgt 1140  
 ggtggcattc atctaattctg ttgactgtcct gaatagaaga aaaacacaga agaaggagc 1200  
 atttactgtc tacatgactg catggatg acactgtatct tttctgcct ttggactggg 1260  
 atttactt ggtgcctctg attctcaggc ttccagagtt ggatcagaac ttacaacatc 1320  
 aggtctagtt ctcagccat cagacatagt ttggaaactac atcaccacct ttccatgtc 1380  
 tccacattgc acacagcaga ttcccagcct ccataattgt gtgtatcaac tacttaata 1440  
 cattctcaca cacacacaca cacacacaca cacacacaca cacacataca ccatttgcc 1500  
 ttttctctg aagaactctg acaaataca gatttggta ctgaaagaga ttctagagga 1560  
 acgaaatttt aaggataaat ttctgaatt ggttatgggg tttctgaat tggctctata 1620  
 atctaatttag atataaaatt ctggtaactt tatttacaat aataaagata gcactatgt 1680  
 ttcaaa 1686

&lt;210&gt; 148

&lt;211&gt; 347

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 148

Met	Ala	Leu	Leu	Phe	Ser	Leu	Ile	Leu	Ala	Ile	Cys	Thr	Arg	Pro	Gly
1															
														10	
															15

Phe	Leu	Ala	Ser	Pro	Ser	Gly	Val	Arg	Leu	Val	Gly	Gly	Leu	His	Arg
													20		30

Cys	Glu	Gly	Arg	Val	Glu	Val	Glu	Gln	Lys	Gly	Gln	Trp	Gly	Thr	Val
												35		45	

Cys	Asp	Asp	Gly	Trp	Asp	Ile	Lys	Asp	Val	Ala	Val	Leu	Cys	Arg	Glu
												50		60	

Leu	Gly	Cys	Gly	Ala	Ala	Ser	Gly	Thr	Pro	Ser	Gly	Ile	Leu	Tyr	Glu
												65		80	

Pro	Pro	Ala	Glu	Lys	Glu	Gln	Lys	Val	Leu	Ile	Gln	Ser	Val	Ser	Cys
												85		95	

Thr	Gly	Thr	Glu	Asp	Thr	Leu	Ala	Gln	Cys	Glu	Gln	Glu	Val	Tyr
												100		110

Asp Cys Ser His Asp Glu Asp Ala Gly Ala Ser Cys Glu Asn Pro Glu  
 115 120 125

Ser Ser Phe Ser Pro Val Pro Glu Gly Val Arg Leu Ala Asp Gly Pro  
 130 135 140

Gly His Cys Lys Gly Arg Val Glu Val Lys His Gln Asn Gln Trp Tyr  
 145 150 155 160

Thr Val Cys Gln Thr Gly Trp Ser Leu Arg Ala Ala Lys Val Val Cys  
 165 170 175

Arg Gln Leu Gly Cys Gly Arg Ala Val Leu Thr Gln Lys Arg Cys Asn  
 180 185 190

Lys His Ala Tyr Gly Arg Lys Pro Ile Trp Leu Ser Gln Met Ser Cys  
 195 200 205

Ser Gly Arg Glu Ala Thr Leu Gln Asp Cys Pro Ser Gly Pro Trp Gly  
 210 215 220

Lys Asn Thr Cys Asn His Asp Glu Asp Thr Trp Val Glu Cys Glu Asp  
 225 230 235 240

Pro Phe Asp Leu Arg Leu Val Gly Gly Asp Asn Leu Cys Ser Gly Arg  
 245 250 255

Leu Glu Val Leu His Lys Gly Val Trp Gly Ser Val Cys Asp Asp Asn  
 260 265 270

Trp Gly Glu Lys Glu Asp Gln Val Val Cys Lys Gln Leu Gly Cys Gly  
 275 280 285

Lys Ser Leu Ser Pro Ser Phe Arg Asp Arg Lys Cys Tyr Gly Pro Gly  
 290 295 300

Val Gly Arg Ile Trp Leu Asp Asn Val Arg Cys Ser Gly Glu Glu Gln  
 305 310 315 320

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Ser Leu Glu Gln Cys Gln His Arg Phe Trp Gly Phe His Asp Cys Thr  
 325 330 335

His Gln Glu Asp Val Ala Val Ile Cys Ser Val  
 340 345

<210> 149  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic

### **oligonucleotide probe**

<400> 149  
 ttcagctcat cacccatccc tgcc

24

<210> 150  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 150  
 ggctcataca aaataccact aggg

24

<210> 151  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 151  
 gggcctccac cgctgtgaag ggcgggtgga ggttggaaacag aaaggccagt

50

<210> 152  
 <211> 1427  
 <212> DNA  
 <213> Homo sapiens

<400> 152  
 actgcactcg gttctatcga ttgaattccc cggggatcct ctagagatcc ctgcaccccg  
 acccaacgcgt ccgcggacgc gtggggggac gcgtggggcg gctaccagga agagtctgcc 120  
 gaaggtgaag gccatggact tcatacaccc cacagccatc ctgccccctgc tggtcgctg 180  
 cctggggctc ttccggctct tccggctgct gcagtgggtg cgcgggaagg cctacctcg 240  
 gaatgtgtg gtgggtatca caggccac ctcagggctg ggcaaagaat gtgc当地  
 cttctatgtt ggggtgtata aactgggtct ctgtggcccg aatgggtgggg ccctagaaga 360  
 gctcatcaga gaacttaccg cttctatgc caccaggatc cagacacaca agccttactt 420  
 ggtgacccctc gacctcacag actctgggc catagttca gcagcagctg agatcctgca 480  
 gtgtttggc tatgtcgaca tacttgtcaa caatgttggg atcagctacc gtggtaccat 540  
 catggacacc acagtggatg tggacaagag ggtcatggag acaaactact ttggcccg 600  
 tgctctaacc aaagcactcc tgccctccat gatcaagagg agccaaggcc acattgtcgc 660  
 catcagcgc atccaggcc agatgagcat tcctttcga tcagcatatg cagccctccaa 720  
 gcacgcaacc caggcttct ttgactgtct gcgtggcccg atgaaacagt atgaaattga 780  
 ggtgaccgtc atcagccccg gtcacatcca caccacccctc tctgtaaatg ccatcaccgc 840  
 ggtatggatct aggtatggag ttatggacac caccacagcc caggcccgaa gccctgtgga 900  
 ggtggcccg gatgttctg ctgctgtggg gaagaagaag aaagatgtga tcttgctga 960  
 cttaactgcct tccttgctg tttatctcg aactctgtct cctggctct tcttcagcc 1020  
 catggccccc agggccagaa aagagcggaa atccaaagaaatcctagtact ctgaccagcc 1080

agggccaggc cagagaagca gcactcttag gcttgcttac tctacaaggg acagttgcac 1140  
 ttgtttagac tttaatggag atttgtctca caagtggaa agactgaaga aacacatctc 1200  
 gtgcagatct gctggcagag gacaatcaa aacgacaaca agctcttcc cagggtgagg 1260  
 ggaaacactt aaggaataaa tatggagctg gggtttaaca ctaaaaaacta gaaataaaca 1320  
 tctcaaacag taaaaaaaaaaa aaaaaagggc ggccgcgact cttagactcg a cctgcagaag 1380  
 ctggccgccc atggccaac ttgttattt cagcttataa tggttac 1427

<210> 153

<211> 310

<212> PRT

<213> Homo sapiens

<400> 153  
 Met Asp Phe Ile Thr Ser Thr Ala Ile Leu Pro Leu Leu Phe Gly Cys  
 1 5 10 15

Leu Gly Val Phe Gly Leu Phe Arg Leu Leu Gln Trp Val Arg Gly Lys  
 20 25 30

Ala Tyr Leu Arg Asn Ala Val Val Ile Thr Gly Ala Thr Ser Gly  
 35 40 45

Leu Gly Lys Glu Cys Ala Lys Val Phe Tyr Ala Ala Gly Ala Lys Leu  
 50 55 60

Val Leu Cys Gly Arg Asn Gly Gly Ala Leu Glu Glu Leu Ile Arg Glu  
 65 70 75 80

Leu Thr Ala Ser His Ala Thr Lys Val Gln Thr His Lys Pro Tyr Leu  
 85 90 95

Val Thr Phe Asp Leu Thr Asp Ser Gly Ala Ile Val Ala Ala Ala  
 100 105 110

Glu Ile Leu Gln Cys Phe Gly Tyr Val Asp Ile Leu Val Asn Asn Ala  
 115 120 125

Gly Ile Ser Tyr Arg Gly Thr Ile Met Asp Thr Thr Val Asp Val Asp  
 130 135 140

Lys Arg Val Met Glu Thr Asn Tyr Phe Gly Pro Val Ala Leu Thr Lys  
 145 150 155 160

Ala Leu Leu Pro Ser Met Ile Lys Arg Arg Gln Gly His Ile Val Ala  
 165 170 175

Ile Ser Ser Ile Gln Gly Lys Met Ser Ile Pro Phe Arg Ser Ala Tyr  
 180 185 190

Ala Ala Ser Lys His Ala Thr Gln Ala Phe Phe Asp Cys Leu Arg Ala  
 195 200 205

Glu Met Glu Gln Tyr Glu Ile Glu Val Thr Val Ile Ser Pro Gly Tyr

210

215

220

Ile His Thr Asn Leu Ser Val Asn Ala Ile Thr Ala Asp Gly Ser Arg  
225                    230                    235                    240

Tyr Gly Val Met Asp Thr Thr Ala Gln Gly Arg Ser Pro Val Glu  
245                    250                    255

Val Ala Gln Asp Val Leu Ala Ala Val Gly Lys Lys Lys Asp Val  
260                    265                    270

Ile Leu Ala Asp Leu Leu Pro Ser Leu Ala Val Tyr Leu Arg Thr Leu  
275                    280                    285

Ala Pro Gly Leu Phe Phe Ser Leu Met Ala Ser Arg Ala Arg Lys Glu  
290                    295                    300

Arg Lys Ser Lys Asn Ser  
305                    310

<210> 154

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 154

ggtgctaaac tggtgctctg tggc

24

<210> 155

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 155

cagggcaaga tgagcattcc

20

<210> 156

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 156  
 tcatactgtt ccatctcgcc acgc  
 24

<210> 157  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 157  
 aatgggtgggg ccctagaaga gtcacatcaga gaactcacccg cttctcatgc 50

<210> 158  
 <211> 1771  
 <212> DNA  
 <213> Homo sapiens

<400> 158  
 cccacgcgtc cgctgggttt agatcgagca accctctaaa agcagtttag agtggtaaaa 60  
 aaaaaaaaaaa acacaccaaa cgctcgccgc cacaagggtt atgaaatttc ttctggacat 120  
 cctcctgttt ctcccggttac tgatcgcttg ctcccttagag tccttcgtga agcttttat 180  
 tcctaagagg agaaaatcg tcaccggcga aatcggtctg attacaggag ctgggcattgg 240  
 aattgggaga ctgactgcct atgaatttgc taaacttaaa agcaagctgg ttctctggga 300  
 tataaataag catggactgg aggaaacacgc tgccaaatgc aaggactgg gtgccaaagg 360  
 tcataccctt gtggtagact gcagcaaccg agaagatatt tacagctctg caaagaagg 420  
 gaaggcagaa attggagatg ttagtatttt agtaaataat gctgggttag tctatacatc 480  
 agatttggtt gctacacaag atcctcagat tgaaaagact tttgaagttt atgtacttgc 540  
 acatttctgg actacaaaagg catttcttcc tgcaatgacg aagaataacc atggccatat 600  
 tgtcaactgtg gcttcggcag ctggacatgt ctgggtcccc ttcttactgg ctactgttc 660  
 aagcaagttt gctgctgtt gatttcataa aactttgaca gatgaactgg ctgccttaca 720  
 aataaactggaa gtcaaaaacaa catgtctgtg tcctaatttc gtaaacactg gttcatcaa 780  
 aaatccaagt acaagttgg gaccactct ggaacctgag gaagtggtaa acaggctgat 840  
 gcatggatt ctgactgagc agaagatgtat ttttattcca tcttctatag cttttttaac 900  
 aacattggaa aggatccttc ctgagcgttt cttggcagtt ttaaaacgaa aaatcgtgt 960  
 taagttgtat gcagtttattt gatataaaaat gaaagcgc当地 taagcaccta gtttctgaa 1020  
 aactgattt ccagggtttag gttgatgtca tctaataatgtt ccagaatttt aatgtttgaa 1080  
 ctctgtttt ttcttaattt cccatttttca tcaatatcat ttttgaggct ttggcagtct 1140  
 tcatttacta ccacttgttcc tttagccaaa agotgattac atatgatata aacagagaaaa 1200  
 tacctttaga ggtgacttta agaaaaatgtt agaaaaaagaa cccaaatgac tttttaaaaa 1260  
 taatttccaa gattattttgt ggctcacctg aaggctttgc aaaatttgc ccataaccgt 1320  
 ttattnaaca tatatttttta ttttgatttgc cacttaattt ttgtataattt tggtttctt 1380  
 ttctgtttt acataaaaatc agaaaacttca agtctctaa ataaaaatgaa ggactatatc 1440  
 tagtggattt tcacaatgaa tatcatgaa tctcaatggg taggttcat cctaccatt 1500  
 gccactctgtt ttccgttggat atacctcaca ttccaatgcc aaacatttct gcacaggaa 1560  
 gcttagagggtt gatacacgtt ttgcaagttt aaaaagcatca ctgggatttt aggagaattt 1620  
 agagaatgtt cccacaaaatg gcagcaataa taaatggatc acactttaaa aaaaaaaaaaa 1680  
 aaaaaaaaaaa aaaaaaaaaaa aaaaaaaaaaa aaaaaaaaaaa aaaaaaaaaaa aaaaaaaaaaa 1740  
 aaaaaaaaaaa aaaaaaaaaaa aaaaaaaaaaa a a 1771

<210> 159

&lt;211&gt; 300

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 159

Met	Lys	Phe	Leu	Leu	Asp	Ile	Leu	Leu	Leu	Leu	Pro	Leu	Leu	Ile	Val
1			5				10							15	

Cys	Ser	Leu	Glu	Ser	Phe	Val	Lys	Leu	Phe	Ile	Pro	Lys	Arg	Arg	Lys
			20				25						30		

Ser	Val	Thr	Gly	Glu	Ile	Val	Leu	Ile	Thr	Gly	Ala	Gly	His	Gly	Ile
			35				40					45			

Gly	Arg	Leu	Thr	Ala	Tyr	Glu	Phe	Ala	Lys	Leu	Lys	Ser	Lys	Leu	Val
			50			55				60					

Leu	Trp	Asp	Ile	Asn	Lys	His	Gly	Leu	Glu	Glu	Thr	Ala	Ala	Lys	Cys
			65			70			75				80		

Lys	Gly	Leu	Gly	Ala	Lys	Val	His	Thr	Phe	Val	Val	Asp	Cys	Ser	Asn
			85			90						95			

Arg	Glu	Asp	Ile	Tyr	Ser	Ser	Ala	Lys	Lys	Val	Lys	Ala	Glu	Ile	Gly
			100				105					110			

Asp	Val	Ser	Ile	Leu	Val	Asn	Asn	Ala	Gly	Val	Val	Tyr	Thr	Ser	Asp
			115			120						125			

Leu	Phe	Ala	Thr	Gln	Asp	Pro	Gln	Ile	Glu	Lys	Thr	Phe	Glu	Val	Asn
			130			135			140						

Val	Leu	Ala	His	Phe	Trp	Thr	Thr	Lys	Ala	Phe	Leu	Pro	Ala	Met	Thr
			145			150			155				160		

Lys	Asn	Asn	His	Gly	His	Ile	Val	Thr	Val	Ala	Ser	Ala	Ala	Gly	His
			165			170						175			

Val	Ser	Val	Pro	Phe	Leu	Leu	Ala	Tyr	Cys	Ser	Ser	Lys	Phe	Ala	Ala
			180			185						190			

Val	Gly	Phe	His	Lys	Thr	Leu	Thr	Asp	Glu	Leu	Ala	Ala	Leu	Gln	Ile
			195			200					205				

Thr	Gly	Val	Lys	Thr	Thr	Cys	Leu	Cys	Pro	Asn	Phe	Val	Asn	Thr	Gly
			210			215					220				

Phe	Ile	Lys	Asn	Pro	Ser	Thr	Ser	Leu	Gly	Pro	Thr	Leu	Glu	Pro	Glu
			225			230			235			240			

Glu	Val	Val	Asn	Arg	Leu	Met	His	Gly	Ile	Leu	Thr	Glu	Gln	Lys	Met
			245			250			255				255		

Ile Phe Ile Pro Ser Ser Ile Ala Phe Leu Thr Thr Leu Glu Arg Ile  
 260 265 270

Leu Pro Glu Arg Phe Leu Ala Val Leu Lys Arg Lys Ile Ser Val Lys  
 275 280 285

Phe Asp Ala Val Ile Gly Tyr Lys Met Lys Ala Gln  
 290 295 300

<210> 160  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 160  
ggtaaggca gaaattggag atg 23

<210> 161  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 161  
atcccatgca tcagcctgtt tacc 24

<210> 162  
<211> 48  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 162  
gctggtag tctatacatc agattttttt gctacacaag atcctcag 48

<210> 163  
<211> 2076  
<212> DNA  
<213> Homo sapiens

<400> 163  
cccacgcgtc cgccggacgcg tggtcgact agttctagat cgcgagcgcc cggccggc 60  
tcagggagga gcaccgactg cgccgcaccc tgagagatgg ttggtgccat gtgaaagg 120

attgttcgc tggcctgtt gatgcctggc ccctgtgatg ggctgtttcg ctccctatac 180  
 agaagtgtt ccatgccacc taaggagac tcaggacagc cattatttct cacccttac 240  
 attgaagctg ggaagatcca aaaaggaaga gaattgagtt tggcggccc ttcccagga 300  
 ctgaacatga agagttatgc cggttcctc accgtaaata agacttacaa cagcaacctc 360  
 ttcttcttgt tctcccaagc tcagatacag ccagaagatg ccccagtagt tctctggcta 420  
 cagggtggc cgggagggttc atccatgtt ggactcttg tggAACATGG gccttatgtt 480  
 gtcacaagta acatgacctt gcgtacaga gacttcccct ggaccacaac gctctccatg 540  
 ctttacattg acaatccagt gggcacaggc ttcagttta ctgtatgatac ccacggatat 600  
 gcagtcaatg aggacgatgt agcacggat ttatacagtg cactaattca gttttccag 660  
 atatttcctg aatataaaaa taatgacttt tatgtcactg gggagtctta tgcaggaaa 720  
 tatgtgccag ccattgcaca cctcatccat tccctcaacc ctgtgagaga ggtgaagatc 780  
 aacctgaacg gaattgctat tggagatgga tattctgatc cccaatcaat tataggggc 840  
 tatgcagaat tcctgtacca aattggctt ttggatgaga agcaaaaaaa gtacttccag 900  
 aagcagtgcc atgaatgcat agaacacatc aggaagcaga actggttga ggccttgaa 960  
 atactggata aactactaga tggcgactta acaagtgatc cttcttactt ccagaatgtt 1020  
 acaggatgta gtaattacta taacttttg cggtgcacgg aacctgagga tcagctttac 1080  
 tatgtgaaat ttttgtcact cccagaggtg agacaagcca tccacgtgg gaatcagact 1140  
 ttaatgatg gaactatagt tgaaaagtac ttgcgagaag atacagtaca gtcagttaaag 1200  
 ccatggttaa ctgaaatcat gaataattat aaggttctga tctacaatgg ccaactggac 1260  
 atcatcgtgg cagctgcct gacagagcgc tccttgatgg gcatggactg gaaaggatcc 1320  
 caggaataca agaaggcaga aaaaaaagtt tggagatct ttaaatctga cagtgaagtg 1380  
 gctggttaca tccggcaagc gggtgacttc catcaggtaa ttattcgagg tggaggacat 1440  
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 taacaaacaa agctgtaaaca tcttttctg ccaataacag aagttggca tgccgtgaag 1920  
 gtgtttggaa atattattgg ataagaatag ctcaattatc ccaaataaaat ggatgaagct 1980  
 ataatagtt tggggaaaaag attctcaaataat gtataaagtc tttagaacaaa agaattcttt 2040  
 gaaataaaaaa tattatatat aaaagtaaaa aaaaaaa 2076

<210> 164  
 <211> 476  
 <212> PRT  
 <213> Homo sapiens

<400> 164

Met	Val	Gly	Ala	Met	Trp	Lys	Val	Ile	Val	Ser	Leu	Val	Leu	Leu	Met
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Pro	Gly	Pro	Cys	Asp	Gly	Leu	Phe	Arg	Ser	Leu	Tyr	Arg	Ser	Val	Ser
															20
															25
															30

Met	Pro	Pro	Lys	Gly	Asp	Ser	Gly	Gln	Pro	Leu	Phe	Leu	Thr	Pro	Tyr
															35
															40
															45

Ile	Glu	Ala	Gly	Lys	Ile	Gln	Lys	Gly	Arg	Glu	Leu	Ser	Leu	Val	Gly
															50
															55
															60

Pro Phe Pro Gly Leu Asn Met Lys Ser Tyr Ala Gly Phe Leu Thr Val

65	70	75	80
Asn Lys Thr Tyr Asn Ser Asn Leu Phe Phe Trp Phe Pro Ala Gln			
85		90	95
Ile Gln Pro Glu Asp Ala Pro Val Val Leu Trp Leu Gln Gly Gly Pro			
100		105	110
Gly Gly Ser Ser Met Phe Gly Leu Phe Val Glu His Gly Pro Tyr Val			
115		120	125
Val Thr Ser Asn Met Thr Leu Arg Asp Arg Asp Phe Pro Trp Thr Thr			
130		135	140
Thr Leu Ser Met Leu Tyr Ile Asp Asn Pro Val Gly Thr Gly Phe Ser			
145		150	155
Phe Thr Asp Asp Thr His Gly Tyr Ala Val Asn Glu Asp Asp Val Ala			
165		170	175
Arg Asp Leu Tyr Ser Ala Leu Ile Gln Phe Phe Gln Ile Phe Pro Glu			
180		185	190
Tyr Lys Asn Asn Asp Phe Tyr Val Thr Gly Glu Ser Tyr Ala Gly Lys			
195		200	205
Tyr Val Pro Ala Ile Ala His Leu Ile His Ser Leu Asn Pro Val Arg			
210		215	220
Glu Val Lys Ile Asn Leu Asn Gly Ile Ala Ile Gly Asp Gly Tyr Ser			
225		230	235
240			
Asp Pro Glu Ser Ile Ile Gly Gly Tyr Ala Glu Phe Leu Tyr Gln Ile			
245		250	255
Gly Leu Leu Asp Glu Lys Gln Lys Lys Tyr Phe Gln Lys Gln Cys His			
260		265	270
Glu Cys Ile Glu His Ile Arg Lys Gln Asn Trp Phe Glu Ala Phe Glu			
275		280	285
Ile Leu Asp Lys Leu Leu Asp Gly Asp Leu Thr Ser Asp Pro Ser Tyr			
290		295	300
Phe Gln Asn Val Thr Gly Cys Ser Asn Tyr Tyr Asn Phe Leu Arg Cys			
305		310	315
320			
Thr Glu Pro Glu Asp Gln Leu Tyr Tyr Val Lys Phe Leu Ser Leu Pro			
325		330	335
Glu Val Arg Gln Ala Ile His Val Gly Asn Gln Thr Phe Asn Asp Gly			
340		345	350

Thr Ile Val Glu Lys Tyr Leu Arg Glu Asp Thr Val Gln Ser Val Lys  
 355 360 365

Pro Trp Leu Thr Glu Ile Met Asn Asn Tyr Lys Val Leu Ile Tyr Asn  
 370 375 380

Gly Gln Leu Asp Ile Ile Val Ala Ala Ala Leu Thr Glu Arg Ser Leu  
 385 390 395 400

Met Gly Met Asp Trp Lys Gly Ser Gln Glu Tyr Lys Lys Ala Glu Lys  
 405 410 415

Lys Val Trp Lys Ile Phe Lys Ser Asp Ser Glu Val Ala Gly Tyr Ile  
 420 425 430

Arg Gln Ala Gly Asp Phe His Gln Val Ile Ile Arg Gly Gly His  
 435 440 445

Ile Leu Pro Tyr Asp Gln Pro Leu Arg Ala Phe Asp Met Ile Asn Arg  
 450 455 460

Phe Ile Tyr Gly Lys Gly Trp Asp Pro Tyr Val Gly  
 465 470 475

<210> 165  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 165  
 ttccatgcc a cctaaggag actc 24

<210> 166  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 166  
 tggatgagg gtgcaatggc tggc 24

<210> 167  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
       oligonucleotide probe  
  
 <400> 167  
       agctctcaga ggctggtcac aggg 24  
  
 <210> 168  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
       oligonucleotide probe  
  
 <400> 168  
       gtcgccctt tcccaggact gaacatgaag agttatgccg gcttcctcac 50  
  
 <210> 169  
 <211> 2477  
 <212> DNA  
 <213> Homo sapiens  
  
 <400> 169  
       cgagggctt tccggctccg gaatggcaca tgtggaaat ccagtcttgt tggctacaac 60  
       attttccct ttcttaacaa gttctaacag ctgttctaac agctagtgtat cagggttct 120  
       tcttgcttga gaagaaaagg ctgagggcag agcagggcac tctcaactca ggtgaccagc 180  
       tccttgcctc tctgtggata acagagcatg agaaagtcaa gagatgcagg ggagttaggt 240  
       gatgaaagtc taaaatagga aggaattttg tgtcaatat cagactctgg gagcagttga 300  
       cctggagagc ctgggggagg gcctgcctaa caagcttca aaaaacagga gcgacttcca 360  
       ctgggctggg ataagacgt ccgttaggat agggaaagact gggttagtc ctaatatcaa 420  
       attgactggc tgggtgaact tcaacagcct ttaacctct ctgggagatg aaaacgatgg 480  
       cttaaggggc cagaaataga gatgcttgc taaaataat ttaaaaaaaaa gcaagtattt 540  
       tatacgataa aggctagaga caaaaataga taacaggatt ccctgaacat tcctaagagg 600  
       gagaaagtat gttaaaaata gaaaaaccaa aatgcagaag gaggagactc acagagctaa 660  
       accaggatgg ggaccctggg tcaggccagc ctcttgcct ctcccgaaaa ttattttgg 720  
       tctgaccact ctgccttgc ttttgcagaa tcatgtgagg gccaaccggg gaaggtggag 780  
       cagatgagca cacacaggag ccgtctcctc accggccccc ctctcagcat ggaacagagg 840  
       cagccctggc cccggggccct ggaggtggac agccgcctcg tggctctgcct ctcagtggc 900  
       tgggtgctgc tggccccccc agcagccggc atgcctcagt tcagcacctt ccactctgag 960  
       aatcgtgact ggaccttcaa ccacttgacc gtccaccaag ggacgggggc cgtctatgt 1020  
       ggggccatca accgggtcta taagctgaca ggcaacctga ccatccaggt ggctcataag 1080  
       acaggggccag aagaggacaa caagtctcg taccggcccc tcatgtgca gcccgcagc 1140  
       gaagtgctca ccctcaccaa caatgtcaac aagctgtca tcattgacta ctctgagaac 1200  
       cgcctgctgg cctgtggag cctctaccag ggggtctgca agctgtgcg gctggatgac 1260  
       ctcttcattcc tggtgagcc atcccacaag aaggagact acctgtccag tgtcaacaag 1320  
       acgggcacca tgtacgggtt gattgtgcgc tctgagggtg aggtggcaa gctcttcattc 1380  
       ggcacggctg tggatggaa gcaggattac ttcccaccc tggcagccg gaagctgccc 1440  
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       ctcatcaaga tcccttcaga caccctggcc ctggtctccc actttgacat ttctcacatc 1560  
       tacggctttg ctatgtgggg ctttgtctac tttctcaactg tccagcccgaa gaccctgag 1620  
       ggtgtggcca tcaactccgc tggagacctc ttctcacaccc caccgcacatcg 1680

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acatctqcaa	aagcaaa					2477

<210> 170

<211> 552

<212> PRT

<213> Homo sapiens

<400> 170

Met Gly Thr Leu Gly Gln Ala Ser Leu Phe Ala Pro Pro Gly Asn Tyr  
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Phe Trp Ser Asp His Ser Ala Leu Cys Phe Ala Glu Ser Cys Glu Gly  
20 25 30

Gln Pro Gly Lys Val Glu Gln Met Ser Thr His Arg Ser Arg Leu Leu  
35 40 45

Thr Ala Ala Pro Leu Ser Met Glu Gln Arg Gln Pro Trp Pro Arg Ala  
                   50                  55                          60

Leu Glu Val Asp Ser Arg Ser Val Val Leu Leu Ser Val Val Trp Val  
65 . . . . . 70 . . . . . 75 . . . . . 80

Leu Leu Ala Pro Pro Ala Ala Gly Met Pro Gln Phe Ser Thr Phe His  
85 90 95

Ser Glu Asn Arg Asp Trp Thr Phe Asn His Leu Thr Val His Gln Gly  
100 105 110

Thr Gly Ala Val Tyr Val Gly Ala Ile Asn Arg Val Tyr Lys Leu Thr  
115 120 125

Gly Asn Leu Thr Ile Gln Val Ala His Lys Thr Gly Pro Glu Glu Asp  
130 135 140

Asn Lys Ser Arg Tyr Pro Pro Leu Ile Val Gln Pro Cys Ser Glu Val  
 115 150 155 160

Leu Thr Leu Thr Asn Asn Val Asn Lys Leu Leu Ile Ile Asp Tyr Ser  
165 170 175

Glu Asn Arg Leu Leu Ala Cys Gly Ser Leu Tyr Gln Gly Val Cys Lys  
 180 185 190

Leu Leu Arg Leu Asp Asp Leu Phe Ile Leu Val Glu Pro Ser His Lys  
 195 200 205

Lys Glu His Tyr Leu Ser Ser Val Asn Lys Thr Gly Thr Met Tyr Gly  
 210 215 220

Val Ile Val Arg Ser Glu Gly Glu Asp Gly Lys Leu Phe Ile Gly Thr  
 225 230 235 240

Ala Val Asp Gly Lys Gln Asp Tyr Phe Pro Thr Leu Ser Ser Arg Lys  
 245 250 255

Leu Pro Arg Asp Pro Glu Ser Ser Ala Met Leu Asp Tyr Glu Leu His  
 260 265 270

Ser Asp Phe Val Ser Ser Leu Ile Lys Ile Pro Ser Asp Thr Leu Ala  
 275 280 285

Leu Val Ser His Phe Asp Ile Phe Tyr Ile Tyr Gly Phe Ala Ser Gly  
 290 295 300

Gly Phe Val Tyr Phe Leu Thr Val Gln Pro Glu Thr Pro Glu Gly Val  
 305 310 315 320

Ala Ile Asn Ser Ala Gly Asp Leu Phe Tyr Thr Ser Arg Ile Val Arg  
 325 330 335

Leu Cys Lys Asp Asp Pro Lys Phe His Ser Tyr Val Ser Leu Pro Phe  
 340 345 350

Gly Cys Thr Arg Ala Gly Val Glu Tyr Arg Leu Leu Gln Ala Ala Tyr  
 355 360 365

Leu Ala Lys Pro Gly Asp Ser Leu Ala Gln Ala Phe Asn Ile Thr Ser  
 370 375 380

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Gln Asp Asp Val Leu Phe Ala Ile Phe Ser Lys Gly Gln Lys Gln Tyr  
 385 390 395 400

His His Pro Pro Asp Asp Ser Ala Leu Cys Ala Phe Pro Ile Arg Ala  
 405 410 415

Ile Asn Leu Gln Ile Lys Glu Arg Leu Gln Ser Cys Tyr Gln Gly Glu  
 420 425 430

Gly Asn Leu Glu Leu Asn Trp Leu Leu Gly Lys Asp Val Gln Cys Thr  
 435 440 445

Lys Ala Pro Val Pro Ile Asp Asp Asn Phe Cys Gly Leu Asp Ile Asn

100

450                    455                    460  
Gln Pro Leu Gly Gly Ser Thr Pro Val Glu Gly Leu Thr Leu Tyr Thr  
465                    470                    475                    480  
Thr Ser Arg Asp Arg Met Thr Ser Val Ala Ser Tyr Val Tyr Asn Gly  
485                    490                    495  
Tyr Ser Val Val Phe Val Gly Thr Lys Ser Gly Lys Leu Lys Lys Val  
500                    505                    510  
Arg Val Tyr Glu Phe Arg Cys Ser Asn Ala Ile His Leu Leu Ser Lys  
515                    520                    525  
Glu Ser Leu Leu Glu Gly Ser Tyr Trp Trp Arg Phe Asn Tyr Arg Gln  
530                    535                    540  
Leu Tyr Phe Leu Gly Glu Gln Arg  
545                    550

<210> 171  
<211> 20  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Description of Artificial Sequence: Synthetic  
      oligonucleotide probe  
  
<400> 171  
tggaataccg cctcctgcag                    20  
  
<210> 172  
<211> 24  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Description of Artificial Sequence: Synthetic  
      oligonucleotide probe  
  
<400> 172  
cttctgccct ttggagaaga tggc                    24  
  
<210> 173  
<211> 43  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Description of Artificial Sequence: Synthetic  
      oligonucleotide probe

<400> 173  
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 <210> 174  
 <211> 3106  
 <212> DNA  
 <213> Homo sapiens  
  
 <220>  
 <221> modified\_base  
 <222> (1683)  
 <223> a, t, c or g  
  
 <400> 174  
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 aacacgcgt gaccacgtgg agectccggc ggaggccgc cgcacgctg ggactccgtc 120  
 tgctggctgt ctgggcttc ctgggtctcc gcaggctgga ctggagcacc ctggccctc 180  
 tgcggctccg ccatcgacag ctggggctgc aggccaaggg ctggacttc atgctggagg 240  
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 ggagggaccg cctgctgaag atgaaggcct gtggctgaa caccctcacc acctatgttc 360  
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 aggcttcgt cctgtatggcc gcagagatcg ggctgtgggt gattctgcgt ccaggcccc 480  
 acatctgcag tgagatggac ctgggggct tgcccaagctg gctactccaa gaccctggca 540  
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 tggagaatga atatggttcc tataataaag accccgcata catgccctac gtcaagaagg 720  
 cactggagga ccgtggcatt gtggaaactgc tcctgacttcc agacaacaag gatgggctga 780  
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 caggtccctg gttgagcagc ggaatcaacc aggtcatcg ttttgaggag acgtatggcgg 1920  
 gcccgcatt acagttcacg gaaacccccc acctggcagc gaaccagtac attaagttag 1980  
 cggcggcacc ccctctgtc ggtgccagtggagactgcc gcctccctt gacctgaagc 2040  
 ctggtgctg ctggcccccacc cctcaactgca aaagcatctc cttaagttagc aacctcagg 2100  
 actggggctc acagtctgac cctgtctcag ctcaaaaccc taagcctgca gggaaaggtg 2160  
 ggtggctct gggctggct ttgtttagtga tggcttccct acagccctgc tcttctgccc 2220  
 aggtgtcggt gctgtctcta gggggggagc agctaattcag atcgcccagc ctggccct 2280

cagaaaaagt gctgaaacgt gcccttgcac cggacgtcac agccctgcga gcatctgctg 2340  
 gactcaggcg tgctcttgc tggccttgg gaggcttggc cacatccctc atggccccc 2400  
 tttatccccg aaatcctgg tgtgtcacca gtgttagaggg tggggaaagggt gtgtctcacc 2460  
 tgagctgact ttgttcttc ttccacaacct tctgagcctt cttgggatt ctgaaaggaa 2520  
 ctccgggtga gaaacatgtg acttccccctt tcccttcca ctcgctgctt cccacagggt 2580  
 gacaggctgg gctggagaaa cagaaatcct caccctgcgt cttcccaagt tagcagggt 2640  
 ctctgggttt cagtggggag gacatgtgag tcctggcaga accatggcc catgtctgca 2700  
 catccaggaa ggaggacaga agggccagct cacatgtgag tcctggcaga accatggcc 2760  
 catgtctgca catccaggaa ggaggacaga agggccagct cacatgtgag tcctggcaga 2820  
 agccatggcc catgtctgca catccaggaa ggaggacaga agggccagct cacatgtgag 2880  
 tcctggcaga agccatggcc catgtctgca catccaggaa ggaggacaga agggccagct 2940  
 cagtggcccc cgctccccac ccccaacgcc cgaacagcag gggcagagca gccctcc 3000  
 gaagtgtgtc caagtccgca ttgagcctt gttctgggc ccagcccaac acctggctt 3060  
 ggctcaactgt cctgagttgc agtaaagcta taaccttcaa tcacaa 3106

&lt;210&gt; 175

&lt;211&gt; 636

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; MOD\_RES

&lt;222&gt; (539)

&lt;223&gt; Any amino acid

&lt;400&gt; 175

Met	Thr	Thr	Trp	Ser	Leu	Arg	Arg	Arg	Pro	Ala	Arg	Thr	Leu	Gly	Leu
1					5							10			15

Leu	Leu	Leu	Val	Val	Leu	Gly	Phe	Leu	Val	Leu	Arg	Arg	Leu	Asp	Trp
					20				25				30		

Ser	Thr	Leu	Val	Pro	Leu	Arg	Leu	Arg	His	Arg	Gln	Leu	Gly	Leu	Gln
					35				40			45			

Ala	Lys	Gly	Trp	Asn	Phe	Met	Leu	Glu	Asp	Ser	Thr	Phe	Trp	Ile	Phe
					50			55			60				

Gly	Gly	Ser	Ile	His	Tyr	Phe	Arg	Val	Pro	Arg	Glu	Tyr	Trp	Arg	Asp
					65			70		75		80			

Arg	Leu	Leu	Lys	Met	Lys	Ala	Cys	Gly	Leu	Asn	Thr	Leu	Thr	Thr	Tyr
					85				90			95			

Val	Pro	Trp	Asn	Leu	His	Glu	Pro	Glu	Arg	Gly	Lys	Phe	Asp	Phe	Ser
					100			105			110				

Gly	Asn	Leu	Asp	Leu	Glu	Ala	Phe	Val	Leu	Met	Ala	Ala	Glu	Ile	Gly
					115			120			125				

Leu	Trp	Val	Ile	Leu	Arg	Pro	Gly	Pro	Tyr	Ile	Cys	Ser	Glu	Met	Asp
					130			135			140				

Leu Gly Gly Leu Pro Ser Trp Leu Leu Gln Asp Pro Gly Met Arg Leu  
 145 150 155 160  
 Arg Thr Thr Tyr Lys Gly Phe Thr Glu Ala Val Asp Leu Tyr Phe Asp  
 165 170 175  
 His Leu Met Ser Arg Val Val Pro Leu Gln Tyr Lys Arg Gly Gly Pro  
 180 185 190  
 Ile Ile Ala Val Gln Val Glu Asn Glu Tyr Gly Ser Tyr Asn Lys Asp  
 195 200 205  
 Pro Ala Tyr Met Pro Tyr Val Lys Lys Ala Leu Glu Asp Arg Gly Ile  
 210 215 220  
 Val Glu Leu Leu Leu Thr Ser Asp Asn Lys Asp Gly Leu Ser Lys Gly  
 225 230 235 240  
 Ile Val Gln Gly Val Leu Ala Thr Ile Asn Leu Gln Ser Thr His Glu  
 245 250 255  
 Leu Gln Leu Leu Thr Thr Phe Leu Phe Asn Val Gln Gly Thr Gln Pro  
 260 265 .270  
 Lys Met Val Met Glu Tyr Trp Thr Gly Trp Phe Asp Ser Trp Gly Gly  
 275 280 285  
 Pro His Asn Ile Leu Asp Ser Ser Glu Val Leu Lys Thr Val Ser Ala  
 290 295 300  
 Ile Val Asp Ala Gly Ser Ser Ile Asn Leu Tyr Met Phe His Gly Gly  
 305 310 315 320  
 Thr Asn Phe Gly Phe Met Asn Gly Ala Met His Phe His Asp Tyr Lys  
 325 330 335  
 Ser Asp Val Thr Ser Tyr Asp Tyr Asp Ala Val Leu Thr Glu Ala Gly  
 340 345 350  
 Asp Tyr Thr Ala Lys Tyr Met Lys Leu Arg Asp Phe Phe Gly Ser Ile  
 355 360 365  
 Ser Gly Ile Pro Leu Pro Pro Pro Asp Leu Leu Pro Lys Met Pro  
 370 375 380  
 Tyr Glu Pro Leu Thr Pro Val Leu Tyr Leu Ser Leu Trp Asp Ala Leu  
 385 390 395 400  
 Lys Tyr Leu Gly Glu Pro Ile Lys Ser Glu Lys Pro Ile Asn Met Glu  
 405 410 415  
 Asn Leu Pro Val Asn Gly Gly Asn Gly Gln Ser Phe Gly Tyr Ile Leu  
 420 425 430

Tyr Glu Thr Ser Ile Thr Ser Ser Gly Ile Leu Ser Gly His Val His  
 435 440 445  
 Asp Arg Gly Gln Val Phe Val Asn Thr Val Ser Ile Gly Phe Leu Asp  
 450 455 460  
 Tyr Lys Thr Thr Lys Ile Ala Val Pro Leu Ile Gln Gly Tyr Thr Val  
 465 470 475 480  
 Leu Arg Ile Leu Val Glu Asn Arg Gly Arg Val Asn Tyr Gly Glu Asn  
 485 490 495  
 Ile Asp Asp Gln Arg Lys Gly Leu Ile Gly Asn Leu Tyr Leu Asn Asp  
 500 505 510  
 Ser Pro Leu Lys Asn Phe Arg Ile Tyr Ser Leu Asp Met Lys Lys Ser  
 515 520 525  
 Phe Phe Gln Arg Phe Gly Leu Asp Lys Trp Xaa Ser Leu Pro Glu Thr  
 530 535 540  
 Pro Thr Leu Pro Ala Phe Phe Leu Gly Ser Leu Ser Ile Ser Ser Thr  
 545 550 555 560  
 Pro Cys Asp Thr Phe Leu Lys Leu Glu Gly Trp Glu Lys Gly Val Val  
 565 570 575  
 Phe Ile Asn Gly Gln Asn Leu Gly Arg Tyr Trp Asn Ile Gly Pro Gln  
 580 585 590  
 Lys Thr Leu Tyr Leu Pro Gly Pro Trp Leu Ser Ser Gly Ile Asn Gln  
 595 600 605  
 Val Ile Val Phe Glu Glu Thr Met Ala Gly Pro Ala Leu Gln Phe Thr  
 610 615 620  
 Glu Thr Pro His Leu Gly Arg Asn Gln Tyr Ile Lys  
 625 630 635

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<210> 176  
 <211> 2505  
 <212> DNA  
 <213> Homo sapiens

<400> 176  
 ggggacgcgg agctgagagg ctccgggcta gctaggtgta ggggtggacg ggtcccagga 60  
 ccctggtag ggttctctac ttggccttcg gtgggggtca agacgcaggc acctacgcca 120  
 aaggggagca aagccgggct cggcccaggc cccccaggac ctccatctcc caatgttgg 180  
 ggaatccgac acgtgacggt ctgtccgccc tctcagacta gaggagcgct gtaaacgcca 240  
 tggctcccaa gaagctgtcc tgccctcggt ccctgctgct gccgctcagc ctgacgctac 300  
 tgctgccccca ggcagacact cggtcggtcg tagtgatag gggtcatgac cggtttctcc 360  
 tagacggggc cccgttccgc tatgtgtctg gcagcctgca ctactttcgg gtaccgcggg 420

tgcttggc cgaccggc ttgaagatgc gatggagcgg cctcaacgcc atacagttt 480  
 atgtccctg gaactaccac gaccacagc ctgggtcta taacttaat ggcagccgg 540  
 acctcattgc ctttctgaat gaggcagtc tagcAACCT gtggcata ctgagaccag 600  
 gacccatcat ctgtcagag tggagatgg ggggtctccc atcctggttt ctgcggaaac 660  
 ctgaaattca tctaagaacc tcagatccag acttccttgc cgcagtggac tcctggttca 720  
 aggtcttgct gccccagata tatccatggc tttatcacaa tggggcaac atcattagca 780  
 ttcaggtgga gaatgaatat ggtagctaca gagcctgtga cttcagctac atgaggcact 840  
 tggctggct cttccgtca ctgctaggag aaaagatctt gctcttcacc acagatggc 900  
 ctgaaggact caagtgtggc tccctccggg gactctatac cactgttagat ttggcccg 960  
 ctgacaacat gaccaaatac ttacccctgc ttccgaagta tgaacccat gggccattgg 1020  
 taaactctga gtactacaca ggctggctgg attactggg ccagaatcac tccacacgg 1080  
 ctgtgtcagc tptaaccaaa ggactagaga acatgctcaa gttgggagcc agtgtgaaca 1140  
 tgtacatgtt ccatggaggt accaactttg gatattggaa tggcgtccgat aagaaggac 1200  
 gcttccttcc gattactacc agctatgact atgatgcacc tatatctgaa gcaggggacc 1260  
 ccacacctaa gcttttgc cttcgagatg tcacagcaa gttccagggaa gttccttgg 1320  
 gacccattacc tccccccgagc cccaaagatga tgcttgacc tggactctg cacctgggg 1380  
 ggcatttact ggcttccta gacttgc tt gccccgtgg gccattcat tcaatcttc 1440  
 caatgaccc ttgaggctgtc aaggcaggacc atggctcat gttgtaccga accttatatga 1500  
 cccataccat ttttggcca acaccattct ggggtccaaa taatggagtc catgaccgtg 1560  
 cctatgtat ggtggatggg gtgttccagg gtgttggaa gcgaaatatg agagacaaac 1620  
 tattttgac ggggaaactg ggggtccaaac tggatatctt ggtggagaac atggggaggc 1680  
 tcagcttgg gtctaacagc agtgacttca agggcctgtt gaagccacca attctggggc 1740  
 aaacaatct tacccagtgg atgatgttcc ctctgaaaat tgataaacctt gtgaagtgg 1800  
 ggttccctt ccagttggca aaatggccat atcctcaagc tcctctggc cccacattct 1860  
 actccaaac atttccaatt ttaggctcag ttggggacac atttctatat ctacctggat 1920  
 ggaccaaggg ccaagtctgg atcaatgggt ttaacttggg ccgtactgg acaaagcagg 1980  
 ggccacaaca gaccctctac gtcccaagat tcctgcgtt tccttagggg gcccctaaca 2040  
 aaattacatt gctggacta gaagatgtac ctctccagcc ccaagtccaa tttttggata 2100  
 agcctatctt caatgactact agtactttgc acaggacaca tatcaattcc ctccagctg 2160  
 atacactgag tgcctctgaa ccaatggagt taagtggca ctgaaaggta ggccgggcat 2220  
 ggtggctcat gcctgtatc ccagcacttt gggaggctga gacgggtggaa ttacctgagg 2280  
 tcagacttc aagaccagcc tggccaaacat ggtgaaaccc cgtctccact aaaaatacaa 2340  
 aaattagccg ggcgtatgg tggcacctc taatccagc tacttgggag gctgagggca 2400  
 ggagaattgc ttgaatccag gaggcagagg ttgcagttag tgaggttgtt accactgcac 2460  
 tccagcctgg ctgacagtga gacactccat ctcaaaaaaa aaaaa 2505

<210> 177  
 <211> 654  
 <212> PRT  
 <213> Homo sapiens

<400> 177  
 Met Ala Pro Lys Lys Leu Ser Cys Leu Arg Ser Leu Leu Leu Pro Leu  
 1 5 10 15

Ser Leu Thr Leu Leu Pro Gln Ala Asp Thr Arg Ser Phe Val Val  
 20 25 30

Asp Arg Gly His Asp Arg Phe Leu Leu Asp Gly Ala Pro Phe Arg Tyr  
 35 40 45

Val Ser Gly Ser Leu His Tyr Phe Arg Val Pro Arg Val Leu Trp Ala  
 50 55 60

Asp Arg Leu Leu Lys Met Arg Trp Ser Gly Leu Asn Ala Ile Gln Phe  
 65                    70                    75                    80  
 Tyr Val Pro Trp Asn Tyr His Glu Pro Gln Pro Gly Val Tyr Asn Phe  
 85                    90                    95  
 Asn Gly Ser Arg Asp Leu Ile Ala Phe Leu Asn Glu Ala Ala Leu Ala  
 100                    105                    110  
 Asn Leu Leu Val Ile Leu Arg Pro Gly Pro Tyr Ile Cys Ala Glu Trp  
 115                    120                    125  
 Glu Met Gly Gly Leu Pro Ser Trp Leu Leu Arg Lys Pro Glu Ile His  
 130                    135                    140  
 Leu Arg Thr Ser Asp Pro Asp Phe Leu Ala Ala Val Asp Ser Trp Phe  
 145                    150                    155                    160  
 Lys Val Leu Leu Pro Lys Ile Tyr Pro Trp Leu Tyr His Asn Gly Gly  
 165                    170                    175  
 Asn Ile Ile Ser Ile Gln Val Glu Asn Glu Tyr Gly Ser Tyr Arg Ala  
 180                    185                    190  
 Cys Asp Phe Ser Tyr Met Arg His Leu Ala Gly Leu Phe Arg Ala Leu  
 195                    200                    205  
 Leu Gly Glu Lys Ile Leu Leu Phe Thr Thr Asp Gly Pro Glu Gly Leu  
 210                    215                    220  
 Lys Cys Gly Ser Leu Arg Gly Leu Tyr Thr Val Asp Phe Gly Pro  
 225                    230                    235                    240  
 Ala Asp Asn Met Thr Lys Ile Phe Thr Leu Leu Arg Lys Tyr Glu Pro  
 245                    250                    255  
 His Gly Pro Leu Val Asn Ser Glu Tyr Tyr Thr Gly Trp Leu Asp Tyr  
 260                    265                    270  
 Trp Gly Gln Asn His Ser Thr Arg Ser Val Ser Ala Val Thr Lys Gly  
 275                    280                    285  
 Leu Glu Asn Met Leu Lys Leu Gly Ala Ser Val Asn Met Tyr Met Phe  
 290                    295                    300  
 His Gly Gly Thr Asn Phe Gly Tyr Trp Asn Gly Ala Asp Lys Lys Gly  
 305                    310                    315                    320  
 Arg Phe Leu Pro Ile Thr Thr Ser Tyr Asp Tyr Asp Ala Pro Ile Ser  
 325                    330                    335  
 Glu Ala Gly Asp Pro Thr Pro Lys Leu Phe Ala Leu Arg Asp Val Ile

340	345	350
Ser Lys Phe Gln Glu Val Pro Leu Gly Pro Leu Pro Pro Pro Ser Pro		
355	360	365
Lys Met Met Leu Gly Pro Val Thr Leu His Leu Val Gly His Leu Leu		
370	375	380
Ala Phe Leu Asp Leu Leu Cys Pro Arg Gly Pro Ile His Ser Ile Leu		
385	390	395
Pro Met Thr Phe Glu Ala Val Lys Gln Asp His Gly Phe Met Leu Tyr		
405	410	415
Arg Thr Tyr Met Thr His Thr Ile Phe Glu Pro Thr Pro Phe Trp Val		
420	425	430
Pro Asn Asn Gly Val His Asp Arg Ala Tyr Val Met Val Asp Gly Val		
435	440	445
Phe Gln Gly Val Val Glu Arg Asn Met Arg Asp Lys Leu Phe Leu Thr		
450	455	460
Gly Lys Leu Gly Ser Lys Leu Asp Ile Leu Val Glu Asn Met Gly Arg		
465	470	475
Leu Ser Phe Gly Ser Asn Ser Ser Asp Phe Lys Gly Leu Leu Lys Pro		
485	490	495
Pro Ile Leu Gly Gln Thr Ile Leu Thr Gln Trp Met Met Phe Pro Leu		
500	505	510
Lys Ile Asp Asn Leu Val Lys Trp Trp Phe Pro Leu Gln Leu Pro Lys		
515	520	525
Trp Pro Tyr Pro Gln Ala Pro Ser Gly Pro Thr Phe Tyr Ser Lys Thr		
530	535	540
Phe Pro Ile Leu Gly Ser Val Gly Asp Thr Phe Leu Tyr Leu Pro Gly		
545	550	555
Trp Thr Lys Gly Gln Val Trp Ile Asn Gly Phe Asn Leu Gly Arg Tyr		
565	570	575
Trp Thr Lys Gln Gly Pro Gln Gln Thr Leu Tyr Val Pro Arg Phe Leu		
580	585	590
Leu Phe Pro Arg Gly Ala Leu Asn Lys Ile Thr Leu Leu Glu Leu Glu		
595	600	605
Asp Val Pro Leu Gln Pro Gln Val Gln Phe Leu Asp Lys Pro Ile Leu		
610	615	620

Asn Ser Thr Ser Thr Leu His Arg Thr His Ile Asn Ser Leu Ser Ala  
625 630 635 640

Asp Thr Leu Ser Ala Ser Glu Pro Met Glu Leu Ser Gly His  
645 650

<210> 178  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 178  
tggctactcc aagaccctgg catg 24

<210> 179  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 179  
tggacaaaatc cccttgatca gccc 24

<210> 180  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 180  
gggcatttacc gaaggcgtgg acctttatcc tgaccacctg atgtccagg 50

<210> 181  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 181  
ccagctatga ctatgtatgc cc 22

<210> 182  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 182  
 tggcacccag aatggtgttg gctc 24

<210> 183  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 183  
 cgagatgtca tcagcaagtt ccaggaagtt ccttgggac cttaacctcc 50

<210> 184  
 <211> 1947  
 <212> DNA  
 <213> Homo sapiens

<400> 184  
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 gcaccaccaa tatggcttac atggaaaaa agcttctcat cagttacata tccattattt 120  
 gtgttatgg ctatctgc ctctacactc tcttcgtt attcaggata ccttgaagg 180  
 aatattctt cgaaaaagtc agagaagaga gcagtttag tgacattcca gatgtaaaaa 240  
 acgatttgc gttccttctt cacatggtag accagtatga ccagctatat tccaaagcggtt 300  
 ttgggtgttt cttgtcagaa gtttagtggaaa ataaaacttag gggaaatttagt ttgaaccatg 360  
 agtggacatt tgaaaaactc aggacgaca tttcacgcaa cggccaggac aagcaggagt 420  
 tgcattctgtt catgctgtcg ggggtccccg atgctgtctt tgacctcaca gacctggatg 480  
 tgctaaagct tgaactaatt ccagaagcta aaattcctgc taagatttct caaatgacta 540  
 accttcaaga gctccaccc tgccactgccc ctgcggaaatg tgaacagact gcttttagct 600  
 ttcttcgcga tcacttgaga tgccctcacg tgaagttcac tgatgtggct gaaattcctg 660  
 cctgggtgtt tttgtcaaaa aacccctcgag agttgtactt aataggcaat ttgaactctg 720  
 aaaacaataa gatgatagga cttaatctc tccggagatggt gccggcacctt aagattctcc 780  
 acgtgaagag caatttgacc aaagttccct ccaacattac agatgtggct ccacatctta 840  
 caaagtttagt cattcataat gacggcacta aactcttggt actgaacacgc cttaaagaaaa 900  
 tgatgaatgt cgctgagctg gaactccaga actgtgagct agagagaatc ccacatgcta 960  
 ttttcagcct ctcttaattt caggaactgg attttaagtc caataacatt cgccacaattt 1020  
 agggaaatcat cagtttccag cattttaaac gactgacttg tttaaaaatta tggcataaca 1080  
 aaattgttac tattcctccc tcttattaccc atgtcaaaaa cttggagtc ctttatttct 1140  
 ctaacaacaa gctcgaatcc ttaccagtgg cagttattag ttacagaaaa ctcagatgct 1200  
 tagatgtgag ctacaacaac atttcaatga ttccaaataga aataggattt cttcagaacc 1260  
 tgcagcattt gcataatcact gggaaacaaatggacattctt gccaaaacaaatgtttaat 1320

gcataaagtt gaggacttg aatctggac agaactgcat cacctcactc ccagagaaaag 1380  
 ttggtcagct ctcccagtc actcagctgg agctgaaggg gaactgcttg gaccgcctgc 1440  
 cagcccagct gggccagttt cgatgctca agaaaaagcgg gcttgggtgtt gaagatcacc 1500  
 ttttgatac cctgccactc gaagtcaaag aggcatgaa tcaagacata aatattccct 1560  
 ttgcaaatgg gatttaact aagataatat atgcacagtg atgtgcagga acaacttcct 1620  
 agattgcaag tgctcacgta caagttttaa caagataatg catttttagga gtagatacat 1680  
 cttttaaaat aaaacagaga ggatgcata gaaatgcataa ctgaatgttc 1740  
 aatgttgta gggtttaag tcatttcattt ccaaatttattt tttttttttc ttttggggaa 1800  
 agggaggaa aaattataat cactaatctt ggttctttt aaattgtttt taacttggat 1860  
 gctgccgcta ctgaatgtttt acaaatttgc tgcctgctaa agtaaatgtat taaattgaca 1920  
 ttttcttact aaaaaaaaaaaaaaaa 1947

&lt;210&gt; 185

&lt;211&gt; 501

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 185

Met	Ala	Tyr	Met	Leu	Lys	Lys	Leu	Leu	Ile	Ser	Tyr	Ile	Ser	Ile	Ile
1				5				10					15		

Cys	Val	Tyr	Gly	Phe	Ile	Cys	Leu	Tyr	Thr	Leu	Phe	Trp	Leu	Phe	Arg
				20				25				30			

Ile	Pro	Leu	Lys	Glu	Tyr	Ser	Phe	Glu	Lys	Val	Arg	Glu	Glu	Ser	Ser
				35			40				45				

Phe	Ser	Asp	Ile	Pro	Asp	Val	Lys	Asn	Asp	Phe	Ala	Phe	Leu	Leu	His
			50			55				60					

Met	Val	Asp	Gln	Tyr	Asp	Gln	Leu	Tyr	Ser	Lys	Arg	Phe	Gly	Val	Phe
	65				70				75			80			

Leu	Ser	Glu	Val	Ser	Glu	Asn	Lys	Leu	Arg	Glu	Ile	Ser	Leu	Asn	His
			85					90				95			

Glu	Trp	Thr	Phe	Glu	Lys	Leu	Arg	Gln	His	Ile	Ser	Arg	Asn	Ala	Gln
			100			105			110						

Asp	Lys	Gln	Glu	Leu	His	Leu	Phe	Met	Leu	Ser	Gly	Val	Pro	Asp	Ala
			115			120			125						

Val	Phe	Asp	Leu	Thr	Asp	Leu	Asp	Val	Leu	Lys	Leu	Glu	Leu	Ile	Pro
			130			135				140					

Glu	Ala	Lys	Ile	Pro	Ala	Lys	Ile	Ser	Gln	Met	Thr	Asn	Leu	Gln	Glu
			145			150			155			160			

Leu	His	Leu	Cys	His	Cys	Pro	Ala	Lys	Val	Glu	Gln	Thr	Ala	Phe	Ser
			165			170						175			

Phe	Leu	Arg	Asp	His	Leu	Arg	Cys	Leu	His	Val	Lys	Phe	Thr	Asp	Val
			180			185						190			

Ala Glu Ile Pro Ala Trp Val Tyr Leu Leu Lys Asn Leu Arg Glu Leu  
195 200 205

Tyr Leu Ile Gly Asn Leu Asn Ser Glu Asn Asn Lys Met Ile Gly Leu  
210 215 220

Glu Ser Leu Arg Glu Leu Arg His Leu Lys Ile Leu His Val Lys Ser  
225 230 235 240

Asn Leu Thr Lys Val Pro Ser Asn Ile Thr Asp Val Ala Pro His Leu  
245 250 255

Thr Lys Leu Val Ile His Asn Asp Gly Thr Lys Leu Leu Val Leu Asn  
260 265 270

Ser Leu Lys Lys Met Met Asn Val Ala Glu Leu Glu Leu Gln Asn Cys  
275 280 285

Glu Leu Glu Arg Ile Pro His Ala Ile Phe Ser Leu Ser Asn Leu Gln  
290 295 300

Glu Leu Asp Leu Lys Ser Asn Asn Ile Arg Thr Ile Glu Glu Ile Ile  
305 310 315 320

Ser Phe Gln His Leu Lys Arg Leu Thr Cys Leu Lys Leu Trp His Asn  
325 330 335

Lys Ile Val Thr Ile Pro Pro Ser Ile Thr His Val Lys Asn Leu Glu  
340 345 350

Ser Leu Tyr Phe Ser Asn Asn Lys Leu Glu Ser Leu Pro Val Ala Val  
355 360 365

Phe Ser Leu Gln Lys Leu Arg Cys Leu Asp Val Ser Tyr Asn Asn Ile  
370 375 380

Ser Met Ile Pro Ile Glu Ile Gly Leu Leu Gln Asn Leu Gln His Leu  
385 390 395 400

---

His Ile Thr Gly Asn Lys Val Asp Ile Leu Pro Lys Gln Leu Phe Lys  
405 410 415

Cys Ile Lys Leu Arg Thr Leu Asn Leu Gly Gln Asn Cys Ile Thr Ser  
420 425 430

Leu Pro Glu Lys Val Gly Gln Leu Ser Gln Leu Thr Gln Leu Glu Leu  
435 440 445

Lys Gly Asn Cys Leu Asp Arg Leu Pro Ala Gln Leu Gly Gln Cys Arg  
450 455 460

Met Leu Lys Lys Ser Gly Leu Val Val Glu Asp His Leu Phe Asp Thr

465	470	475	480
Leu Pro Leu Glu Val Lys Glu Ala Leu Asn Gln Asp Ile Asn Ile Pro 485 490 495			
Phe Ala Asn Gly Ile 500			
<210> 186			
<211> 21			
<212> DNA			
<213> Artificial Sequence			
<220>			
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe			
<400> 186			
cctccctcta ttacccatgt c 21			
<210> 187			
<211> 24			
<212> DNA			
<213> Artificial Sequence			
<220>			
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe			
<400> 187			
gaccaacttt ctctggag gagg 24			
<210> 188			
<211> 47			
<212> DNA			
<213> Artificial Sequence			
<220>			
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe			
<400> 188			
gtcacttat ttctctaaca acaagctcg atccttacca gtggcag 47			
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<211> 2917			
<212> DNA			
<213> Homo sapiens			
<400> 189			
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actttttta ttctttttt tccatctctg ggccagcttg ggatcctagg ccgcctcg 120			
aaagacatttg tggtttacac acataaggat ctgtgtttgg ggttttcttctt tccctccctg 180			

<210> 190  
<211> 607  
<212> PRT  
<213> *Homo sapiens*

<400> 190

Met Glu Leu Val Arg Arg Leu Met Pro Leu Thr Leu Leu Ile Leu Ser  
 1 5 10 15

Cys Leu Ala Glu Leu Thr Met Ala Glu Ala Glu Gly Asn Ala Ser Cys  
 20 25 30

Thr Val Ser Leu Gly Gly Ala Asn Met Ala Glu Thr His Lys Ala Met  
 35 40 45

Ile Leu Gln Leu Asn Pro Ser Glu Asn Cys Thr Trp Thr Ile Glu Arg  
 50 55 60

Pro Glu Asn Lys Ser Ile Arg Ile Ile Phe Ser Tyr Val Gln Leu Asp  
 65 70 75 80

Pro Asp Gly Ser Cys Glu Ser Glu Asn Ile Lys Val Phe Asp Gly Thr  
 85 90 95

Ser Ser Asn Gly Pro Leu Leu Gly Gln Val Cys Ser Lys Asn Asp Tyr  
 100 105 110

Val Pro Val Phe Glu Ser Ser Ser Thr Leu Thr Phe Gln Ile Val  
 115 120 125

Thr Asp Ser Ala Arg Ile Gln Arg Thr Val Phe Val Phe Tyr Tyr Phe  
 130 135 140

Phe Ser Pro Asn Ile Ser Ile Pro Asn Cys Gly Gly Tyr Leu Asp Thr  
 145 150 155 160

Leu Glu Gly Ser Phe Thr Ser Pro Asn Tyr Pro Lys Pro His Pro Glu  
 165 170 175

Leu Ala Tyr Cys Val Trp His Ile Gln Val Glu Lys Asp Tyr Lys Ile  
 180 185 190

Lys Leu Asn Phe Lys Glu Ile Phe Leu Glu Ile Asp Lys Gln Cys Lys  
 195 200 205

Phe Asp Phe Leu Ala Ile Tyr Asp Gly Pro Ser Thr Asn Ser Gly Leu  
 210 215 220

Ile Gly Gln Val Cys Gly Arg Val Thr Pro Thr Phe Glu Ser Ser Ser  
 225 230 235 240

Asn Ser Leu Thr Val Val Leu Ser Thr Asp Tyr Ala Asn Ser Tyr Arg  
 245 250 255

Gly Phe Ser Ala Ser Tyr Thr Ser Ile Tyr Ala Glu Asn Ile Asn Thr  
 260 265 270

Thr Ser Leu Thr Cys Ser Ser Asp Arg Met Arg Val Ile Ile Ser Lys  
 275 280 285

Ser Tyr Leu Glu Ala Phe Asn Ser Asn Gly Asn Asn Leu Gln Leu Lys  
 290 295 300  
 Asp Pro Thr Cys Arg Pro Lys Leu Ser Asn Val Val Glu Phe Ser Val  
 305 310 315 320  
 Pro Leu Asn Gly Cys Gly Thr Ile Arg Lys Val Glu Asp Gln Ser Ile  
 325 330 335  
 Thr Tyr Thr Asn Ile Ile Thr Phe Ser Ala Ser Ser Thr Ser Glu Val  
 340 345 350  
 Ile Thr Arg Gln Lys Gln Leu Gln Ile Ile Val Lys Cys Glu Met Gly  
 355 360 365  
 His Asn Ser Thr Val Glu Ile Ile Tyr Ile Thr Glu Asp Asp Val Ile  
 370 375 380  
 Gln Ser Gln Asn Ala Leu Gly Lys Tyr Asn Thr Ser Met Ala Leu Phe  
 385 390 395 400  
 Glu Ser Asn Ser Phe Glu Lys Thr Ile Leu Glu Ser Pro Tyr Tyr Val  
 405 410 415  
 Asp Leu Asn Gln Thr Leu Phe Val Gln Val Ser Leu His Thr Ser Asp  
 420 425 430  
 Pro Asn Leu Val Val Phe Leu Asp Thr Cys Arg Ala Ser Pro Thr Ser  
 435 440 445  
 Asp Phe Ala Ser Pro Thr Tyr Asp Leu Ile Lys Ser Gly Cys Ser Arg  
 450 455 460  
 Asp Glu Thr Cys Lys Val Tyr Pro Leu Phe Gly His Tyr Gly Arg Phe  
 465 470 475 480  
 Gln Phe Asn Ala Phe Lys Phe Leu Arg Ser Met Ser Ser Val Tyr Leu  
 485 490 495  
 Gln Cys Lys Val Leu Ile Cys Asp Ser Ser Asp His Gln Ser Arg Cys  
 500 505 510  
 Asn Gln Gly Cys Val Ser Arg Ser Lys Arg Asp Ile Ser Ser Tyr Lys  
 515 520 525  
 Trp Lys Thr Asp Ser Ile Ile Gly Pro Ile Arg Leu Lys Arg Asp Arg  
 530 535 540  
 Ser Ala Ser Gly Asn Ser Gly Phe Gln His Glu Thr His Ala Glu Glu  
 545 550 555 560  
 Thr Pro Asn Gln Pro Phe Asn Ser Val His Leu Phe Ser Phe Met Val

565

570

575

Leu Ala Leu Asn Val Val Thr Val Ala Thr Ile Thr Val Arg His Phe  
 580 585 590

Val Asn Gln Arg Ala Asp Tyr Lys Tyr Gln Lys Leu Gln Asn Tyr  
 595 600 605

&lt;210&gt; 191

&lt;211&gt; 21

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

&lt;400&gt; 191

tctctattcc aaactgtggc g

21

&lt;210&gt; 192

&lt;211&gt; 22

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

&lt;400&gt; 192

tttgatgacg attcgaaggt gg

22

&lt;210&gt; 193

&lt;211&gt; 47

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

&lt;400&gt; 193

ggaaggatcc ttcaccagcc ccaattaccc aaagccgcac cctgagc

47

&lt;210&gt; 194

&lt;211&gt; 2362

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 194

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 cgggacatgc ggccccagga gctccccagg ctgcgcgttcc cggtgctgtct gttgctgttg 120  
 ctgctgctgc cgccgcccgtgcc cacagcgcca cgcgcgttca cccccacctgg 180

gagttccctgg acgcccggca gctgcccccg cgtagtttgacc agggccaagtt cggcatcttc 240  
atccactggg gagtgtttc cgtccccagg ttccggtagcg aatgggtctg gtggatttgg 300  
aaaaaggaaa agataccgaa gtagtgggaa ttatgaaag ataattaccc tcctagttc 360  
aaatatgaag attttggacc actattaca gaaaaattt ttaatgccaa ccagtgggca 420  
gatattttc aggccctctgg tgccaaatac attgtcttaa cttccaaaca tcatgaaggc 480  
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ctgtactatt cccttttga atggttcat ccgcctttcc ttgaggatga atccagttca 660  
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aacagcacag gtttcttggc ctggttatataatgaaagcc cagttccgggg cacagtagtc 840  
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taaactcatt gtgcaaatgt aa 2362

<210> 195

<211> 467

<212> PRT

<213> Homo sapiens

<400> 195

Met Arg P

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Arg Phe Asp Pro Thr Trp Glu Ser Leu Asp Ala Arg Gln Leu Pro Ala  
35 40 45

Trp Phe Asp Gln Ala Lys Phe Gly Ile Phe His Trp Gly Val Phe  
 50 55 60  
 Ser Val Pro Ser Phe Gly Ser Glu Trp Phe Trp Trp Tyr Trp Gln Lys  
 65 70 75 80  
 Glu Lys Ile Pro Lys Tyr Val Glu Phe Met Lys Asp Asn Tyr Pro Pro  
 85 90 95  
 Ser Phe Lys Tyr Glu Asp Phe Gly Pro Leu Phe Thr Ala Lys Phe Phe  
 100 105 110  
 Asn Ala Asn Gln Trp Ala Asp Ile Phe Gln Ala Ser Gly Ala Lys Tyr  
 115 120 125  
 Ile Val Leu Thr Ser Lys His His Glu Gly Phe Thr Leu Trp Gly Ser  
 130 135 140  
 Glu Tyr Ser Trp Asn Trp Asn Ala Ile Asp Glu Gly Pro Lys Arg Asp  
 145 150 155 160  
 Ile Val Lys Glu Leu Glu Val Ala Ile Arg Asn Arg Thr Asp Leu Arg  
 165 170 175  
 Phe Gly Leu Tyr Tyr Ser Leu Phe Glu Trp Phe His Pro Leu Phe Leu  
 180 185 190  
 Glu Asp Glu Ser Ser Ser Phe His Lys Arg Gln Phe Pro Val Ser Lys  
 195 200 205  
 Thr Leu Pro Glu Leu Tyr Glu Leu Val Asn Asn Tyr Gln Pro Glu Val  
 210 215 220  
 Leu Trp Ser Asp Gly Asp Gly Gly Ala Pro Asp Gln Tyr Trp Asn Ser  
 225 230 235 240  
 Thr Gly Phe Leu Ala Trp Leu Tyr Asn Glu Ser Pro Val Arg Gly Thr  
 245 250 255  
 Val Val Thr Asn Asp Arg Trp Gly Ala Gly Ser Ile Cys Lys His Gly  
 260 265 270  
 Gly Phe Tyr Thr Cys Ser Asp Arg Tyr Asn Pro Gly His Leu Leu Pro  
 275 280 285  
 His Lys Trp Glu Asn Cys Met Thr Ile Asp Lys Leu Ser Trp Gly Tyr  
 290 295 300  
 Arg Arg Glu Ala Gly Ile Ser Asp Tyr Leu Thr Ile Glu Glu Leu Val  
 305 310 315 320  
 Lys Gln Leu Val Glu Thr Val Ser Cys Gly Gly Asn Leu Leu Met Asn  
 325 330 335

Ile Gly Pro Thr Leu Asp Gly Thr Ile Ser Val Val Phe Glu Glu Arg  
 340 345 350

Leu Arg Gln Val Gly Ser Trp Leu Lys Val Asn Gly Glu Ala Ile Tyr  
 355 360 365

Glu Thr Tyr Thr Trp Arg Ser Gln Asn Asp Thr Val Thr Pro Asp Val  
 370 375 380

Trp Tyr Thr Ser Lys Pro Lys Glu Lys Leu Val Tyr Ala Ile Phe Leu  
 385 390 395 400

Lys Trp Pro Thr Ser Gly Gln Leu Phe Leu Gly His Pro Lys Ala Ile  
 405 410 415

Leu Gly Ala Thr Glu Val Lys Leu Leu Gly His Gly Gln Pro Leu Asn  
 420 425 430

Trp Ile Ser Leu Glu Gln Asn Gly Ile Met Val Glu Leu Pro Gln Leu  
 435 440 445

Thr Ile His Gln Met Pro Cys Lys Trp Gly Trp Ala Leu Ala Leu Thr  
 450 455 460

Asn Val Ile  
 465

<210> 196  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 196  
tggtttgacc aggccaagtt cggt

23

<210> 197  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 197  
ggattcatcc tcaaggaaga gcgg

24

<210> 198

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<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe

<400> 198
aacttgagc atcagccact ctgc          24

<210> 199
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe

<400> 199
ttccgtgcc agcttcggta gcgagtggtt ctgggtgtat tggca          45

<210> 200
<211> 2372
<212> DNA
<213> Homo sapiens

<400> 200
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catctgaggt gttccctgg ctctgaaggg gttaggcacga tggccaggtg cttcagcccg 180
gtgttgcctc tcacttccat ctggaccacg aggctctgg tccaaggctc tttgcgtgca 240
gaagagctt ccatccaggt gtcatgcaga attatgggaa tcacccttgt gagcaaaaag 300
gcgaaccacg agctgaattt cacagaagct aaggaggcct gtaggctgct gggactaagt 360
ttggccggca aggaccaagt taaaacagcc ttgaaaagcta gctttgaaac ttgcagctat 420
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gatcccataat tcaacactca aactgcaaca caaacaacag aatttattgt cagtgcacgt 660
acctactcg tggcatcccc ttactctaca atacctggcc ctactactac tcctcctgtc 720
ccagcttcca cttctattcc acggagaaaa aaattgattt gtgtcacaga agttttatg 780
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gctctgaaag agaaaacacgt atccccacctg acatgtcctt ctgagccccgg taagagcaaa 1620  
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caactgttttag aacacacaca cttactttt ctggctctca ccactgctga tattttctct 1860  
aggaaatata ctttacaag taacaaaaat aaaaactctt ataaatttct atttttatct 1920  
gagttacaga aatgattact aaggaagatt actcagtaat ttgtttaaaa agtaataaaa 1980  
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tgtaattgaa tattattcct caaaaaattg cacatagtag aacgctatct gggaaagctat 2100  
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gactaatctt attcattttc tctaatatgg caaccattat aaccttaatt tattattaac 2220  
atacctaaga agtacattgt taccttata taccaaagca cattttaaaa gtgccattaa 2280  
caaatgtatc actagccctc cttttccaa caagaaggga ctgagagatg cagaaatatt 2340  
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<210> 201

<211> 322

<211> 522

<213> Artificial sequence

<220>

<223> Synthetic protein

<400> 201

Met Ala Arg Cys Phe Ser Leu Val Leu Leu Leu Thr Ser Ile Trp Thr  
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20 25 30

Gln Val Ser Cys Arg Ile Met Gly Ile Thr Leu Val Ser Lys Lys Ala  
35 40 45

Asn Gln Gln Leu Asn Phe Thr Glu Ala Lys Glu Ala Cys Arg Leu Leu  
50 55 60

Gly Leu Ser Leu Ala Gly Lys Asp Gln Val Glu Thr Ala Leu Lys Ala  
65 70 75 80

Ser Phe Glu Thr Cys Ser Tyr Gly Trp Val Gly Asp Gly Phe Val Val  
85 90 95

Ile Ser Arg Ile Ser Pro Asn Pro Lys Cys Gly Lys Asn Gly Val Gly  
100 105 110

Val Leu Ile Trp Lys Val Pro Val Ser Arg Gln Phe Ala Ala Tyr Cys  
115 120 125

Tyr Asn Ser Ser Asp Thr Trp Thr Asn Ser Cys Ile Pro Glu Ile Ile  
 130 135 140

Thr Thr Lys Asp Pro Ile Phe Asn Thr Gln Thr Ala Thr Gln Thr Thr  
 145 150 155 160  
 Glu Phe Ile Val Ser Asp Ser Thr Tyr Ser Val Ala Ser Pro Tyr Ser  
 165 170 175  
 Thr Ile Pro Ala Pro Thr Thr Pro Pro Ala Pro Ala Ser Thr Ser  
 180 185 190  
 Ile Pro Arg Arg Lys Lys Leu Ile Cys Val Thr Glu Val Phe Met Glu  
 195 200 205  
 Thr Ser Thr Met Ser Thr Glu Thr Glu Pro Phe Val Glu Asn Lys Ala  
 210 215 220  
 Ala Phe Lys Asn Glu Ala Ala Gly Phe Gly Val Pro Thr Ala Leu  
 225 230 235 240  
 Leu Val Leu Ala Leu Leu Phe Phe Gly Ala Ala Ala Gly Leu Gly Phe  
 245 250 255  
 Cys Tyr Val Lys Arg Tyr Val Lys Ala Phe Pro Phe Thr Asn Lys Asn  
 260 265 270  
 Gln Gln Lys Glu Met Ile Glu Thr Lys Val Val Lys Glu Glu Lys Ala  
 275 280 285  
 Asn Asp Ser Asn Pro Asn Glu Glu Ser Lys Lys Thr Asp Lys Asn Pro  
 290 295 300  
 Glu Glu Ser Lys Ser Pro Ser Lys Thr Thr Val Arg Cys Leu Glu Ala  
 305 310 315 320  
 Glu Val

<210> 202  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 202  
 gagctttcca tccagggtgtc atgc

24

<210> 203  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 203  
 gtcagtgaca gtacctactc gg

22

<210> 204  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 204  
 tggagcagga ggagtagtag tagg

24

<210> 205  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 205  
 aggaggcctg taggctgctg ggactaagtt tggccggcaa ggaccaagtt

50

<210> 206  
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 <212> DNA  
 <213> Homo sapiens

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 <221> modified\_base  
 <222> (973)  
 <223> a, t, c or g

<220>  
 <221> modified\_base  
 <222> (977)  
 <223> a, t, c or g

<220>  
 <221> modified\_base  
 <222> (996)  
 <223> a, t, c or g

<220>  
 <221> modified\_base

&lt;222&gt; (1003)

&lt;223&gt; a, t, c or g

&lt;400&gt; 206

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 acccgagatc catcaactgtg gagacaacata taggcaacat ttcatgttt agtaaagtgg 300  
 ccaacacaat tcttttcttc cgcttgata ttcgcattggg cctactttac atcacactct 360  
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 acttccctt gtgtgttagg acttggagga gaaatccctt ggactttcac taaccctctg 1560  
 acataactccc cacaccaggat ttagggcttt ccgtataaaa aagattggga tttccctttt 1620

&lt;210&gt; 207

&lt;211&gt; 296

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 207

Met Ala Val Leu Ala Pro Leu Ile Ala Leu Val Tyr Ser Val Pro Arg

1 5 10 15

Leu Ser Arg Trp Leu Ala Gln Pro Tyr Tyr Leu Leu Ser Ala Leu Leu  
20 25 30Ser Ala Ala Phe Leu Leu Val Arg Lys Leu Pro Pro Leu Cys His Gly  
35 40 45Leu Pro Thr Gln Arg Glu Asp Gly Asn Pro Cys Asp Phe Asp Trp Arg  
50 55 60Glu Val Glu Ile Leu Met Phe Leu Ser Ala Ile Val Met Met Lys Asn  
65 70 75 80

Arg Arg Ser Ile Thr Val Glu Gln His Ile Gly Asn Ile Phe Met Phe  
 85 90 95  
 Ser Lys Val Ala Asn Thr Ile Leu Phe Phe Arg Leu Asp Ile Arg Met  
 100 105 110  
 Gly Leu Leu Tyr Ile Thr Leu Cys Ile Val Phe Leu Met Thr Cys Lys  
 115 120 125  
 Pro Pro Leu Tyr Met Gly Pro Glu Tyr Ile Lys Tyr Phe Asn Asp Lys  
 130 135 140  
 Thr Ile Asp Glu Glu Leu Glu Arg Asp Lys Arg Val Thr Trp Ile Val  
 145 150 155 160  
 Glu Phe Phe Ala Asn Trp Ser Asn Asp Cys Gln Ser Phe Ala Pro Ile  
 165 170 175  
 Tyr Ala Asp Leu Ser Leu Lys Tyr Asn Cys Thr Gly Leu Asn Phe Gly  
 180 185 190  
 Lys Val Asp Val Gly Arg Tyr Thr Asp Val Ser Thr Arg Tyr Lys Val  
 195 200 205  
 Ser Thr Ser Pro Leu Thr Lys Gln Leu Pro Thr Leu Ile Leu Phe Gln  
 210 215 220  
 Gly Gly Lys Glu Ala Met Arg Arg Pro Gln Ile Asp Lys Lys Gly Arg  
 225 230 235 240  
 Ala Val Ser Trp Thr Phe Ser Glu Glu Asn Val Ile Arg Glu Phe Asn  
 245 250 255  
 Leu Asn Glu Leu Tyr Gln Arg Ala Lys Lys Leu Ser Lys Ala Gly Asp  
 260 265 270  
 Asn Ile Pro Glu Glu Gln Pro Val Ala Ser Thr Pro Thr Thr Val Ser  
 275 280 285  
 Asp Gly Glu Asn Lys Lys Asp Lys  
 290 295

<210> 208  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 208  
 gcttggatat tcgcatgggc ctac

<210> 209  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 209 20  
 tggagacaat atccctgagg

<210> 210  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 210 24  
 aacagttggc cacagcatgg cagg

<210> 211  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 211 50  
 ccattgtga ggaactagaa cgggacaaga gggtcaacttg gattgtggag

<210> 212  
 <211> 1985  
 <212> DNA  
 <213> Homo sapiens

<400> 212  
 ggacagctcg cggccccca gagctctagc cgtcgaggag ctgcctgggg acgtttgcc 60  
 tggggcccca gcctggccc ggtcacccctg gcatgaggag atgggcctgt tgctccttgt 120  
 cccattgtctc ctgctcccc gctcctacgg actgccttc tacaacggct tctactactc 180  
 caacagcgcc aacgaccaga acctaggcaa cggtcatggc aaagacctcc ttaatggagt 240  
 gaagctggtg gtggagacac ccgaggagac cctgttcacc taccaagggg ccagtgttat 300  
 cctgcccctgc cgctaccgct acgagccggc cctggcttcc ccgcggcggt tgctgtcaa 360  
 atggtggaag ctgtcggaga acggggcccc agagaaggac gtgctgggtt ccatcggtt 420  
 gaggcaccgc tccttgggg actaccaagg ccgcgtgcac ctgcggcagg acaaagagca 480  
 tgacgtctcg ctggagatcc agatctgcg gctggaggac tatgggcgtt accgctgtga 540  
 ggtcattgac gggctggagg atgaaagcgg tctgggtggg ctggagctgc ggggtgttgt 600

ctttccttac cagtcccca acggcgcta ccagttcaac ttccacgagg gccagcaggt 660  
 ctgtcagag caggctcggt tggtggcctc ctttgagcag ctctccggg cctgggagga 720  
 gggcctggac tggtaacaacg cgggctggct gcaggatgt acgtgcagt accccatcat 780  
 gttccccgg cagccctgcg gtggcccagg cctggcacct ggctgcgaa gctacggccc 840  
 ccgcacccgc cgccgtcacc getatgtatgt attctgttca gctactgccc tcaagggcg 900  
 ggtgtactac ctggagcacc ctgagaagct gacgctgaca gaggcaaggg aggcctgcca 960  
 ggaagatgtat gccacgatcg ccaaggtggg acagctctt gccgcctggg agttccatgg 1020  
 cctggaccgc tgcgacgctg gctggctggc agatggcagc gtccgctacc ctgtgggtca 1080  
 cccgcattcacttgc cccagagcc tggggtccga agttggct tccccgaccc 1140  
 gcagagccgc ttgtacggtg ttactgtcta cgcgcagcac taggacctgg ggccctcccc 1200  
 tgccgcattc cctcaactggc tgggtattta ttgagtgggtt cgttttccct tgggggttgg 1260  
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 tttttgtaa agcaaacaga accaatgcc tcccttgct cctggatgcc ccactcagg 1380  
 aatcatgctt gtcctccctgg gccatggcg gttttgtggg cttctggagg gttcccgcc 1440  
 atccaggctg gtctccctcc cttaaggagg ttgggtggca gagtgggcgg tggcctgtct 1500  
 agaatgccgc cgggagtcgg ggcatggtgg gcacaggctt ccctggccct cagcctgggg 1560  
 gaagaagagg gcctcggggg cctccggagc tgggcttgg gcctctctg cccacctcta 1620  
 ctctctgtg aagccgtga cccagcttg cccactgagg ggctagggt ggaagccagt 1680  
 tctaggctt caggcgaaat ctgagggaaag gaagaaactc ccctcccccgt tcccctccc 1740  
 ctctcggttc caaagaatct gtttgttgtt catttgttcc tctgtttcc ctgtgtgggg 1800  
 agggccctc aggtgtgtgt actttggaca ataaatggtg ctatgactgc cttccgccaa 1860  
 aaaaaaaaaaaaaaaa aaaaaaaaaaaaaaaa aaaaaaaaaaaaaaaa aaaaaaaaaaaaaaaa 1920  
 aaaaaaaaaaaaaaaa aaaaaaaaaaaaaaaa aaaaaaaaaaaaaaaa aaaaaaaaaaaaaaaa 1980  
 aaaaaaaaaaaaaaaa 1985

aaaaa  
 <210> 213  
 <211> 360  
 <212> PRT  
 <213> Homo sapiens

<400> 213  
 Met Gly Leu Leu Leu Leu Val Pro Leu Leu Leu Pro Gly Ser Tyr  
 1 5 10 15

Gly Leu Pro Phe Tyr Asn Gly Phe Tyr Tyr Ser Asn Ser Ala Asn Asp  
 20 25 30

Gln Asn Leu Gly Asn Gly His Gly Lys Asp Leu Leu Asn Gly Val Lys  
 35 40 45

Leu Val Val Glu Thr Pro Glu Glu Thr Leu Phe Thr Tyr Gln Gly Ala  
 50 55 60

Ser Val Ile Leu Pro Cys Arg Tyr Arg Tyr Glu Pro Ala Leu Val Ser  
 65 70 75 80

Pro Arg Arg Val Arg Val Lys Trp Trp Lys Leu Ser Glu Asn Gly Ala  
 85 90 95

Pro Glu Lys Asp Val Leu Val Ala Ile Gly Leu Arg His Arg Ser Phe  
 100 105 110

Gly Asp Tyr Gln Gly Arg Val His Leu Arg Gln Asp Lys Glu His Asp

115	120	125	
Val Ser Leu Glu Ile Gln Asp Leu Arg Leu Glu Asp Tyr Gly Arg Tyr			
130	135	140	
Arg Cys Glu Val Ile Asp Gly Leu Glu Asp Glu Ser Gly Leu Val Glu			
145	150	155	160
Leu Glu Leu Arg Gly Val Val Phe Pro Tyr Gln Ser Pro Asn Gly Arg			
165	170	175	
Tyr Gln Phe Asn Phe His Glu Gly Gln Gln Val Cys Ala Glu Gln Ala			
180	185	190	
Ala Val Val Ala Ser Phe Glu Gln Leu Phe Arg Ala Trp Glu Glu Gly			
195	200	205	
Leu Asp Trp Cys Asn Ala Gly Trp Leu Gln Asp Ala Thr Val Gln Tyr			
210	215	220	
Pro Ile Met Leu Pro Arg Gln Pro Cys Gly Gly Pro Gly Leu Ala Pro			
225	230	235	240
Gly Val Arg Ser Tyr Gly Pro Arg His Arg Arg Leu His Arg Tyr Asp			
245	250	255	
Val Phe Cys Phe Ala Thr Ala Leu Lys Gly Arg Val Tyr Tyr Leu Glu			
260	265	270	
His Pro Glu Lys Leu Thr Leu Thr Glu Ala Arg Glu Ala Cys Gln Glu			
275	280	285	
Asp Asp Ala Thr Ile Ala Lys Val Gly Gln Leu Phe Ala Ala Trp Lys			
290	295	300	
Phe His Gly Leu Asp Arg Cys Asp Ala Gly Trp Leu Ala Asp Gly Ser			
305	310	315	320
Val Arg Tyr Pro Val Val His Pro His Pro Asn Cys Gly Pro Pro Glu			
325	330	335	
Pro Gly Val Arg Ser Phe Gly Phe Pro Asp Pro Gln Ser Arg Leu Tyr			
340	345	350	
Gly Val Tyr Cys Tyr Arg Gln His			
355	360		

&lt;210&gt; 214

&lt;211&gt; 18

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 214  
tgcttcgcta ctgccctc 18

<210> 215  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 215  
ttcccttgtg ggttggag 18

<210> 216  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 216  
aggcgtggaa gccagttc 18

<210> 217  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 217  
agccagttag gaaatgcg 18

<210> 218  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 218  
tgtccaaagt acacacacct gagg 24

&lt;210&gt; 219

&lt;211&gt; 45

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 219

gatgccacga tcgccaagg gggacagctc tttgccgcct ggaag

45

&lt;210&gt; 220

&lt;211&gt; 1503

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 220

ggagagcgg a gcaaggctgg ataacagggg accgatgatg tggcgaccat cagttctgct 60  
 gcttctgttg ctactgaggg acggggccca ggggaagcca tcccccagacg cagggcctca 120  
 tggccagggg agggtgccacc agggcgcccc cctgagcgac gctccccatg atgacgccc 180  
 cgggaacttc cagtagcacc atgaggctt cctgggacgg gaagtggcca aggaattcga 240  
 ccaactcacc ccagaggaaa gccaggcccc tctggggcgg atcgtggacc gcatggaccg 300  
 cgccggggac ggcgacggct gggtgtcgct ggccgagctt cgcgcgtgga tcgcgcacac 360  
 gcagcagcgg cacatacggg actcgggtgag cgccgcctgg gacacgtacg acacggaccg 420  
 cgacgggcgt gtgggttggg aggagctgca caacgcacc tatggccact acgcgcgg 480  
 tgaagaattt catgacgtgg aggatgcaga gacactacaaa aagatgtgg ctcgggacga 540  
 gcggcggttc cgggtggccg accaggatgg ggactcgatg gccactcgag aggagctgac 600  
 agccttcctg caccggcagg agtccctca catgcgggac atcgtgattt ctgaaaccct 660  
 ggaggacctg gacagaaaca aagatggcta tgtccaggtg gaggagtaca tcgcggatct 720  
 gtactcagcc gagcctgggg aggaggagcc ggcgtgggtg cagacggaga ggcagcagt 780  
 ccgggacttc cgggatctga acaaggatgg gcacctggat gggagtggg tggccactg 840  
 ggtgtgccc cctgcccagg accagccct ggtggaaagcc aaccacctgc tgcacgagag 900  
 cgacacggac aaggatgggc ggctgagcaa agcggaaatc ctggtaatt ggaacatgtt 960  
 tgtgggcagt caggccacca actatggcga ggacctgacc cggcaccacg atgagctgt 1020  
 agcacccgcg acctgcacca gcctcagagg cccgcacaaat gaccggagga gggccgcgt 1080  
 tggctggcc ccctccctgt ccaggccccg caggaggcag atgcagtccc aggcatcctc 1140  
 ctggccctgg gctctcaggg accccctggg tcggctctg tccctgtcac acccccaacc 1200  
 ccaggagggg gctgtcatag tcccagagga taagcaatac ctatttctga ctgagtc 1260  
 cagcccaagac ccagggaccc ttggcccaa gctcagctct aagaaccgc ccaaccctc 1320  
 cagctccaaa tctgagcctc caccacatag actgaaactc coctggcccc agccctctcc 1380  
 tgccctggcct ggcctggac actcctctc tgccaggagg caataaaagc cagcggcggg 1440  
 accttgaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1500  
 1503  
 aaa

&lt;210&gt; 221

&lt;211&gt; 328

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 221

Met Met Trp Arg Pro Ser Val Leu Leu Leu Leu Leu Arg His

1	5	10	15
Gly Ala Gln Gly Lys Pro Ser Pro Asp Ala Gly Pro His Gly Gln Gly			
	20	25	30
Arg Val His Gln Ala Ala Pro Leu Ser Asp Ala Pro His Asp Asp Ala			
	35	40	45
His Gly Asn Phe Gln Tyr Asp His Glu Ala Phe Leu Gly Arg Glu Val			
	50	55	60
Ala Lys Glu Phe Asp Gln Leu Thr Pro Glu Glu Ser Gln Ala Arg Leu			
	65	70	75
Gly Arg Ile Val Asp Arg Met Asp Arg Ala Gly Asp Gly Asp Gly Trp			
	85	90	95
Val Ser Leu Ala Glu Leu Arg Ala Trp Ile Ala His Thr Gln Gln Arg			
	100	105	110
His Ile Arg Asp Ser Val Ser Ala Ala Trp Asp Thr Tyr Asp Thr Asp			
	115	120	125
Arg Asp Gly Arg Val Gly Trp Glu Glu Leu Arg Asn Ala Thr Tyr Gly			
	130	135	140
His Tyr Ala Pro Gly Glu Glu Phe His Asp Val Glu Asp Ala Glu Thr			
	145	150	155
Tyr Lys Lys Met Leu Ala Arg Asp Glu Arg Arg Phe Arg Val Ala Asp			
	165	170	175
Gln Asp Gly Asp Ser Met Ala Thr Arg Glu Glu Leu Thr Ala Phe Leu			
	180	185	190
His Pro Glu Glu Phe Pro His Met Arg Asp Ile Val Ile Ala Glu Thr			
	195	200	205
Leu Glu Asp Leu Asp Arg Asn Lys Asp Gly Tyr Val Gln Val Glu Glu			
	210	215	220
Tyr Ile Ala Asp Leu Tyr Ser Ala Glu Pro Gly Glu Glu Pro Ala			
	225	230	235
Trp Val Gln Thr Glu Arg Gln Gln Phe Arg Asp Phe Arg Asp Leu Asn			
	245	250	255
Lys Asp Gly His Leu Asp Gly Ser Glu Val Gly His Trp Val Leu Pro			
	260	265	270
Pro Ala Gln Asp Gln Pro Leu Val Glu Ala Asn His Leu Leu His Glu			
	275	280	285

Ser Asp Thr Asp Lys Asp Gly Arg Leu Ser Lys Ala Glu Ile Leu Gly  
 290 295 300

Asn Trp Asn Met Phe Val Gly Ser Gln Ala Thr Asn Tyr Gly Glu Asp  
 305 310 315 320

Leu Thr Arg His His Asp Glu Leu  
 325

<210> 222  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 222 20  
 cgcaggccct catggccagg

<210> 223  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 223 18  
 gaaatcctgg gtaattgg

<210> 224  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 224 23  
 gtgcgcggtg ctcacagctc atc

<210> 225  
<211> 44  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 225  
 cccccctgag cgacgctccc ccatgatgac gcccacggga actt 44  
  
 <210> 226  
 <211> 2403  
 <212> DNA  
 <213> Homo sapiens  
  
 <400> 226  
 ggggccttgc ctcccgact cgggcgcagc cgggtggatc tcgaggcagg tgcggagcccc 60  
 gggccggcggg cgccgggtcg agggatccct gacgcctctg tccctgtttc tttgtcgctc 120  
 ccagcctgtc tgcgtcgatt ttggcgcccc cgccctcccc cggtgcgggg ttgcacaccg 180  
 atccctggct tgcgtcgatt tgccgcggag ggcgcctccca gacctagagg ggcgcgtggcc 240  
 tggagcagcg ggtcgctgt gtccctctc ctctgcggcg cgcccgggga tccgaagggt 300  
 gcggggctct gaggaggtga cgccgcggggc ctcccgacc ctggccttgc cgcattctc 360  
 cctctctccc aggtgtgagc agccatcag tcaccatgtc cgcagcctgg atcccgctc 420  
 tcggcctcgg tggcgcttg ctgcgtgtc cggggcccg gggcagcggag ggagccgctc 480  
 ccattgttat cacaatgttt accagaggct tggacatcag gaaagagaaa gcagatgtcc 540  
 tctgcccagg gggctgcct ctggagaaat tctctgtgtc tggaaacata gtatatgtt 600  
 ctgtatcgag catatgtggg gctgtgtcc acaggggagt aatcagcaac tcagggggac 660  
 ctgtacgagt ctatagccta cttggtcgag aaaactattc cttagttagat gccaatggca 720  
 tccagtctca aatgcttttct agatggctgt cttcttcac agtaactaaa ggcaaaagta 780  
 gtacacagga ggcacacagga caagcagtgt ccacagcaca tccaccaaca ggtaaacgc 840  
 taaagaaaac acccgagaag aaaactggca ataaagattt taaagcagac attgcatttc 900  
 tgattgtatgg aagcttaat attgggcagc gccgattaa ttacagaag aatttttgtt 960  
 gaaaagtggc tctaattgtt ggaattggaa cagaaggacc acatgtggc cttgttcaag 1020  
 ccagtgaaca tcccaaata gaattttact tggaaaactt tacatcagcc aaagatgttt 1080  
 tggggccat aaaggaagta gggttcagag gggtaattc caatacagga aaagccttga 1140  
 agcatactgc tcagaaattc ttacggtag atgctggagt aaaaaaggg atccccaaag 1200  
 tgggtgggtt atttattgtat ggttggcctt ctgatgacat cgaggaagca ggcattgtgg 1260  
 ccagagagtt tgggtgtcaat gtatttatac ttctgtggc caagcctatc cctgaagaac 1320  
 tggggatggt tcaggatgtc acatttggc acaaggctgt ctgtcgaaat aatggcttct 1380  
 tctcttacca catgccaac tggtttggca ccacaaaata cgtaaagcct ctgttacaga 1440  
 agctgtgcac tcatgaacaa atgatgtgca gcaagacctg ttataactca gtgaacattt 1500  
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 ttgtttccaa catagccaag acttttggaa tctcgacat tggtgccaaat atagctgtc 1620  
 tacagtttac ttatgtatcg cgcacggagt tcagttcac tgactatagc accaaagaga 1680  
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 ccatttcctt cactgttga aatgtgtttt gcccataaag ggagagcccc aacaagaact 1800  
 tcctagtaat tgcacagat gggcagtcct atgatgtatgt ccaaggccct gcagctgtc 1860  
 cacatgtatgc aggaatcact atcttctctg ttgggtgtggc ttgggcaccc ctggatgacc 1920  
 tggaaagatggatggctaaa cgcaggagt ctcacgctt cttcacaaga gagttcacag 1980  
 gattagaacc aattgtttctt gatgtatca gaggcattt tagagatttc tttagaatccc 2040  
 agcaataatg gtaacatttt gacaactgaa agaaaaagta caaggggatc cagtgtgtaa 2100  
 attgtattct cataataactg aatgcttta gcatactaga atcagataca aaactattaa 2160  
 gtatgtcaac agccatttag gcaaataaagc actccctttaa agccgctgcc ttctggttac 2220  
 aatttacagt gtactttgtt aaaaacactg ctgaggcttc ataatcatgg ctcttagaaa 2280  
 ctcaggaaag aggagataat gtggattaaa accttaagag ttctaaccat gcctactaaa 2340  
 tgcacagata tgcaaatcc atagctcaat aaaagaatct gatacttaga caaaaaaaaa 2400  
 aaa 2403

<210> 227

&lt;211&gt; 550

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 227

Met	Ser	Ala	Ala	Trp	Ile	Pro	Ala	Leu	Gly	Leu	Gly	Val	Cys	Leu	Leu
1					5				10				15		

Leu	Leu	Pro	Gly	Pro	Ala	Gly	Ser	Glu	Gly	Ala	Ala	Pro	Ile	Ala	Ile
							20		25				30		

Thr	Cys	Phe	Thr	Arg	Gly	Leu	Asp	Ile	Arg	Lys	Glu	Lys	Ala	Asp	Val
							35		40			45			

Leu	Cys	Pro	Gly	Gly	Cys	Pro	Leu	Glu	Glu	Phe	Ser	Val	Tyr	Gly	Asn
							50		55			60			

Ile	Val	Tyr	Ala	Ser	Val	Ser	Ser	Ile	Cys	Gly	Ala	Ala	Val	His	Arg
								65	70		75		80		

Gly	Val	Ile	Ser	Asn	Ser	Gly	Gly	Pro	Val	Arg	Val	Tyr	Ser	Leu	Pro
							85		90			95			

Gly	Arg	Glu	Asn	Tyr	Ser	Ser	Val	Asp	Ala	Asn	Gly	Ile	Gln	Ser	Gln
							100		105			110			

Met	Leu	Ser	Arg	Trp	Ser	Ala	Ser	Phe	Thr	Val	Thr	Lys	Gly	Lys	Ser
							115		120			125			

Ser	Thr	Gln	Glu	Ala	Thr	Gly	Gln	Ala	Val	Ser	Thr	Ala	His	Pro	Pro
							130		135			140			

Thr	Gly	Lys	Arg	Leu	Lys	Lys	Thr	Pro	Glu	Lys	Lys	Thr	Gly	Asn	Lys
							145		150			155		160	

Asp	Cys	Lys	Ala	Asp	Ile	Ala	Phe	Leu	Ile	Asp	Gly	Ser	Phe	Asn	Ile
							165		170			175			

Gly	Gln	Arg	Arg	Phe	Asn	Leu	Gln	Lys	Asn	Phe	Val	Gly	Lys	Val	Ala
							180		185			190			

Leu	Met	Leu	Gly	Ile	Gly	Thr	Glu	Gly	Pro	His	Val	Gly	Leu	Val	Gln
							195		200			205			

Ala	Ser	Glu	His	Pro	Lys	Ile	Glu	Phe	Tyr	Leu	Lys	Asn	Phe	Thr	Ser
							210		215			220			

Ala	Lys	Asp	Val	Leu	Phe	Ala	Ile	Lys	Glu	Val	Gly	Phe	Arg	Gly	Gly
							225		230			235		240	

Asn	Ser	Asn	Thr	Gly	Lys	Ala	Leu	Lys	His	Thr	Ala	Gln	Lys	Phe	Phe
							245		250			255			

Thr Val Asp Ala Gly Val Arg Lys Gly Ile Pro Lys Val Val Val Val  
 260 265 270

Phe Ile Asp Gly Trp Pro Ser Asp Asp Ile Glu Glu Ala Gly Ile Val  
 275 280 285

Ala Arg Glu Phe Gly Val Asn Val Phe Ile Val Ser Val Ala Lys Pro  
 290 295 300

Ile Pro Glu Glu Leu Gly Met Val Gln Asp Val Thr Phe Val Asp Lys  
 305 310 315 320

Ala Val Cys Arg Asn Asn Gly Phe Phe Ser Tyr His Met Pro Asn Trp  
 325 330 335

Phe Gly Thr Thr Lys Tyr Val Lys Pro Leu Val Gln Lys Leu Cys Thr  
 340 345 350

His Glu Gln Met Met Cys Ser Lys Thr Cys Tyr Asn Ser Val Asn Ile  
 355 360 365

Ala Phe Leu Ile Asp Gly Ser Ser Ser Val Gly Asp Ser Asn Phe Arg  
 370 375 380

Leu Met Leu Glu Phe Val Ser Asn Ile Ala Lys Thr Phe Glu Ile Ser  
 385 390 395 400

Asp Ile Gly Ala Lys Ile Ala Ala Val Gln Phe Thr Tyr Asp Gln Arg  
 405 410 415

Thr Glu Phe Ser Phe Thr Asp Tyr Ser Thr Lys Glu Asn Val Leu Ala  
 420 425 430

Val Ile Arg Asn Ile Arg Tyr Met Ser Gly Gly Thr Ala Thr Gly Asp  
 435 440 445

Ala Ile Ser Phe Thr Val Arg Asn Val Phe Gly Pro Ile Arg Glu Ser  
 450 455 460

Pro Asn Lys Asn Phe Leu Val Ile Val Thr Asp Gly Gln Ser Tyr Asp  
 465 470 475 480

Asp Val Gln Gly Pro Ala Ala Ala His Asp Ala Gly Ile Thr Ile  
 485 490 495

Phe Ser Val Gly Val Ala Trp Ala Pro Leu Asp Asp Leu Lys Asp Met  
 500 505 510

Ala Ser Lys Pro Lys Glu Ser His Ala Phe Phe Thr Arg Glu Phe Thr  
 515 520 525

Gly Leu Glu Pro Ile Val Ser Asp Val Ile Arg Gly Ile Cys Arg Asp  
 530 535 540

Phe Leu Glu Ser Gln Gln  
545 550

<210> 228  
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<212> DNA  
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<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 228  
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18

<210> 229  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 229  
ctgctgtcca caggggag

18

<210> 230  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 230  
ccttgaagca tactgctc

18

<210> 231  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 231  
gagatagcaa tttccgcc

18

<210> 232

<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 232  
ttcctcaaga gggcagcc 18

<210> 233  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 233  
cttggcacca atgtccgaga tttc 24

<210> 234  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 234  
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<210> 235  
<211> 2586  
<212> DNA  
<213> Homo sapiens

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<400> 235  
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gtcgggggcg cgctgcggg cgcatgcggc agatgcagcg gcttggggcc accctgtgt 180  
gcctgtgtct ggccggcgccg gtccccacgg ccccgccgcg cgctccgacg gcgacctcg 240  
ctccagtcggccg gctctcggatccgcaggaa ggaggccacc ctcaatgaga 300  
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aagagatgga ggcagaagaa gctgctgcta aagcatcatc agaagtgaac ctggcaaact 420  
tacctcccag ctatcacaat gagaccaaca cagacacgaa gtttggaaat aataccatcc 480  
atgtgcaccc agaaattcac aagataacca acaaccagac tggacaaatcg gtctttcag 540  
agacaggatcat ccatctgtg ggagacgaaag aaggcagaag gaggcacaag tgcatcatcg 600  
acgaggactg tggcccgacg atgtactgcc agtttgcacg cttccatcg acctgcacg 660  
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<210> 236

<211> 350

<212> PRT

<213> Homo sapiens

<400> 236

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20 25 30

Lys Pro Gly Pro Ala Leu Ser Tyr Pro Gln Glu Glu Ala Thr Leu Asn  
                  35                 40                 45

Glu Met Phe Arg Glu Val Glu Glu Leu Met Glu Asp Thr Gln His Lys  
50 55 60

Leu Arg Ser Ala Val Glu Glu Met Glu Ala Glu Glu Ala Ala Ala Lys  
65 70 75 80

Ala Ser Ser Glu Val Asn Leu Ala Asn Leu Pro Pro Ser Tyr His Asn  
                   85                         90                         95  
  
 Glu Thr Asn Thr Asp Thr Lys Val Gly Asn Asn Thr Ile His Val His  
                   100                     105                         110  
  
 Arg Glu Ile His Lys Ile Thr Asn Asn Gln Thr Gly Gln Met Val Phe  
                   115                     120                         125  
  
 Ser Glu Thr Val Ile Thr Ser Val Gly Asp Glu Glu Gly Arg Arg Ser  
                   130                     135                         140  
  
 His Glu Cys Ile Ile Asp Glu Asp Cys Gly Pro Ser Met Tyr Cys Gln  
                   145                     150                         155                 160  
  
 Phe Ala Ser Phe Gln Tyr Thr Cys Gln Pro Cys Arg Gly Gln Arg Met  
                   165                     170                         175  
  
 Leu Cys Thr Arg Asp Ser Glu Cys Cys Gly Asp Gln Leu Cys Val Trp  
                   180                     185                         190  
  
 Gly His Cys Thr Lys Met Ala Thr Arg Gly Ser Asn Gly Thr Ile Cys  
                   195                     200                         205  
  
 Asp Asn Gln Arg Asp Cys Gln Pro Gly Leu Cys Cys Ala Phe Gln Arg  
                   210                     215                         220  
  
 Gly Leu Leu Phe Pro Val Cys Thr Pro Leu Pro Val Glu Gly Glu Leu  
                   225                     230                         235                 240  
  
 Cys His Asp Pro Ala Ser Arg Leu Leu Asp Leu Ile Thr Trp Glu Leu  
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 Glu Pro Asp Gly Ala Leu Asp Arg Cys Pro Cys Ala Ser Gly Leu Leu  
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 Cys Gln Pro His Ser His Ser Leu Val Tyr Val Cys Lys Pro Thr Phe  
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 Val Gly Ser Arg Asp Gln Asp Gly Glu Ile Leu Leu Pro Arg Glu Val  
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                   305                     310                         315                 320  
  
 Leu Glu Asp Leu Glu Arg Ser Leu Thr Glu Glu Met Ala Leu Gly Glu  
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<211> 17  
<212> DNA  
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<220>  
<223> Synthetic oligonucleotide probe

<400> 237  
ggagctgcac cccttgc 17

<210> 238  
<211> 49  
<212> DNA  
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<220>  
<223> Synthetic Oligonucleotide Probe

<400> 238  
ggaggactgt gccaccatga gagactcttc aaaccgaagg caaaaattgg 49

<210> 239  
<211> 24  
<212> DNA  
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<220>  
<223> Synthetic Oligonucleotide Probe

<400> 239  
gcagagcgg aatgcagcgg cttg 24

<210> 240  
<211> 18  
<212> DNA  
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<220>  
<223> Synthetic Oligonucleotide Probe

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<400> 240  
ttggcagctt catggagg 18

<210> 241  
<211> 18  
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<220>  
<223> Synthetic Oligonucleotide Probe

<400> 241  
cctggcaaa aatgcaac 18

<210> 242  
<211> 24  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Synthetic Oligonucleotide Probe  
  
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ctccagctcc tggcgcacct cctc 24  
  
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<210> 244  
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<212> DNA  
<213> Homo Sapien  
  
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<210> 245  
<211> 713  
<212> PRT  
<213> Homo Sapien

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20 25 30

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35 40 45

Ser Tyr Arg Glu Ala Thr Thr Val Asp Cys Asn Asp Leu Phe Leu
50 55 60

Thr Ala Val Pro Pro Ala Leu Pro Ala Gly Thr Gln Thr Leu Leu
65 70 75

Leu Gln Ser Asn Ser Ile Val Arg Val Asp Gln Ser Glu Leu Gly
80 85 90

Tyr Leu Ala Asn Leu Thr Glu Leu Asp Leu Ser Gln Asn Ser Phe
95 100 105

Ser Asp Ala Arg Asp Cys Asp Phe His Ala Leu Pro Gln Leu Leu
110 115 120

Ser Leu His Leu Glu Glu Asn Gln Leu Thr Arg Leu Glu Asp His
125 130 135

Ser Phe Ala Gly Leu Ala Ser Leu Gln Glu Leu Tyr Leu Asn His
140 145 150

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Asn Gln Leu Tyr Arg Ile Ala Pro Arg Ala Phe Ser Gly Leu Ser  
 155 160 165  
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 170 175 180  
 Asp Ser Arg Trp Phe Glu Met Leu Pro Asn Leu Glu Ile Leu Met  
 185 190 195  
 Ile Gly Gly Asn Lys Val Asp Ala Ile Leu Asp Met Asn Phe Arg  
 200 205 210  
 Pro Leu Ala Asn Leu Arg Ser Leu Val Leu Ala Gly Met Asn Leu  
 215 220 225  
 Arg Glu Ile Ser Asp Tyr Ala Leu Glu Gly Leu Gln Ser Leu Glu  
 230 235 240  
 Ser Leu Ser Phe Tyr Asp Asn Gln Leu Ala Arg Val Pro Arg Arg  
 245 250 255  
 Ala Leu Glu Gln Val Pro Gly Leu Lys Phe Leu Asp Leu Asn Lys  
 260 265 270  
 Asn Pro Leu Gln Arg Val Gly Pro Gly Asp Phe Ala Asn Met Leu  
 275 280 285  
 His Leu Lys Glu Leu Gly Leu Asn Asn Met Glu Glu Leu Val Ser  
 290 295 300  
 Ile Asp Lys Phe Ala Leu Val Asn Leu Pro Glu Leu Thr Lys Leu  
 305 310 315  
 Asp Ile Thr Asn Asn Pro Arg Leu Ser Phe Ile His Pro Arg Ala  
 320 325 330  
 Phe His His Leu Pro Gln Met Glu Thr Leu Met Leu Asn Asn Asn  
 335 340 345  
 Ala Leu Ser Ala Leu His Gln Gln Thr Val Glu Ser Leu Pro Asn  
 350 355 360  
 Leu Gln Glu Val Gly Leu His Gly Asn Pro Ile Arg Cys Asp Cys  
 365 370 375  
 Val Ile Arg Trp Ala Asn Ala Thr Gly Thr Arg Val Arg Phe Ile  
 380 385 390  
 Glu Pro Gln Ser Thr Leu Cys Ala Glu Pro Pro Asp Leu Gln Arg  
 395 400 405  
 Leu Pro Val Arg Glu Val Pro Phe Arg Glu Met Thr Asp His Cys

410	415	420
Leu Pro Leu Ile Ser Pro Arg Ser Phe Pro Pro Ser Leu Gln Val		
425	430	435
Ala Ser Gly Glu Ser Met Val Leu His Cys Arg Ala Leu Ala Glu		
440	445	450
Pro Glu Pro Glu Ile Tyr Trp Val Thr Pro Ala Gly Leu Arg Leu		
455	460	465
Thr Pro Ala His Ala Gly Arg Arg Tyr Arg Val Tyr Pro Glu Gly		
470	475	480
Thr Leu Glu Leu Arg Arg Val Thr Ala Glu Glu Ala Gly Leu Tyr		
485	490	495
Thr Cys Val Ala Gln Asn Leu Val Gly Ala Asp Thr Lys Thr Val		
500	505	510
Ser Val Val Val Gly Arg Ala Leu Leu Gln Pro Gly Arg Asp Glu		
515	520	525
Gly Gln Gly Leu Glu Leu Arg Val Gln Glu Thr His Pro Tyr His		
530	535	540
Ile Leu Leu Ser Trp Val Thr Pro Pro Asn Thr Val Ser Thr Asn		
545	550	555
Leu Thr Trp Ser Ser Ala Ser Ser Leu Arg Gly Gln Gly Ala Thr		
560	565	570
Ala Leu Ala Arg Leu Pro Arg Gly Thr His Ser Tyr Asn Ile Thr		
575	580	585
Arg Leu Leu Gln Ala Thr Glu Tyr Trp Ala Cys Leu Gln Val Ala		
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Phe Ala Asp Ala His Thr Gln Leu Ala Cys Val Trp Ala Arg Thr		
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Lys Glu Ala Thr Ser Cys His Arg Ala Leu Gly Asp Arg Pro Gly		
620	625	630
Leu Ile Ala Ile Leu Ala Leu Ala Val Leu Leu Leu Ala Ala Gly		
635	640	645
Leu Ala Ala His Leu Gly Thr Gly Gln Pro Arg Lys Gly Val Gly		
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Gly Arg Arg Pro Leu Pro Pro Ala Trp Ala Phe Trp Gly Trp Ser		
665	670	675

Ala Pro Ser Val Arg Val Val Ser Ala Pro Leu Val Leu Pro Trp  
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695 700 705

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<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 246

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<210> 247

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 247

aaacttgtcg atggagacca gctc 24

<210> 248

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 248

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<210> 249

<211> 3401

<212> DNA

<213> Homo Sapien

<400> 249

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 cttccatcag ccctgtcgcc acctggctt tcatgaagag cagacactta 3000  
 gaggctggtc gggaaatgggg aggtcgcccc tgggagggca ggcggtgg 3050  
 ccaagccggt tcccgccct ggccctggaa gtgcacacag cccagtcggc 3100  
 acctggtggc tggaagccaa cctgcttttag atcactcggtt tccccacctt 3150  
 agaagggtcc ccgccttaga tcaatcacgt ggacactaag gcacgtttta 3200  
 gagtctcttg tcttaatgtat tatgtccatc cgtctgtccg tccatttg 3250  
 ttttctgcgt cgtgtcattg gatataatcc tcagaaataa tgcacactag 3300  
 cctctgacaa ccatgaagca aaaatccgtt acatgtgggt ctgaacttgt 3350  
 agactcggtc acagtatcaa ataaaatcta taacagaaaa aaaaaaaaaa 3400

a 3401

<210> 250

<211> 546

<212> PRT

<213> Homo Sapien

<400> 250

Met	Arg	Gln	Thr	Ile	Ile	Lys	Val	Ile	Lys	Phe	Ile	Leu	Ile	Ile	
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Cys	Tyr	Thr	Val	Tyr	Tyr	Val	His	Asn	Ile	Lys	Phe	Asp	Val	Asp	
															30

Cys	Thr	Val	Asp	Ile	Glu	Ser	Leu	Thr	Gly	Tyr	Arg	Thr	Tyr	Arg	
															45

Cys	Ala	His	Pro	Leu	Ala	Thr	Leu	Phe	Lys	Ile	Leu	Ala	Ser	Phe	
															60

Tyr	Ile	Ser	Leu	Val	Ile	Phe	Tyr	Gly	Leu	Ile	Cys	Met	Tyr	Thr	
															75

Leu	Trp	Trp	Met	Leu	Arg	Arg	Ser	Leu	Lys	Lys	Tyr	Ser	Phe	Glu	
															90

Ser	Ile	Arg	Glu	Glu	Ser	Ser	Tyr	Ser	Asp	Ile	Pro	Asp	Val	Lys	
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95	100	105
Asn Asp Phe Ala Phe Met Leu His Leu Ile Asp Gln Tyr Asp Pro		
110	115	120
Leu Tyr Ser Lys Arg Phe Ala Val Phe Leu Ser Glu Val Ser Glu		
125	130	135
Asn Lys Leu Arg Gln Leu Asn Leu Asn Asn Glu Trp Thr Leu Asp		
140	145	150
Lys Leu Arg Gln Arg Leu Thr Lys Asn Ala Gln Asp Lys Leu Glu		
155	160	165
Leu His Leu Phe Met Leu Ser Gly Ile Pro Asp Thr Val Phe Asp		
170	175	180
Leu Val Glu Leu Glu Val Leu Lys Leu Glu Leu Ile Pro Asp Val		
185	190	195
Thr Ile Pro Pro Ser Ile Ala Gln Leu Thr Gly Leu Lys Glu Leu		
200	205	210
Trp Leu Tyr His Thr Ala Ala Lys Ile Glu Ala Pro Ala Leu Ala		
215	220	225
Phe Leu Arg Glu Asn Leu Arg Ala Leu His Ile Lys Phe Thr Asp		
230	235	240
Ile Lys Glu Ile Pro Leu Trp Ile Tyr Ser Leu Lys Thr Leu Glu		
245	250	255
Glu Leu His Leu Thr Gly Asn Leu Ser Ala Glu Asn Asn Arg Tyr		
260	265	270
Ile Val Ile Asp Gly Leu Arg Glu Leu Lys Arg Leu Lys Val Leu		
275	280	285
Arg Leu Lys Ser Asn Leu Ser Lys Leu Pro Gln Val Val Thr Asp		
290	295	300
Val Gly Val His Leu Gln Lys Leu Ser Ile Asn Asn Glu Gly Thr		
305	310	315
Lys Leu Ile Val Leu Asn Ser Leu Lys Lys Met Ala Asn Leu Thr		
320	325	330
Glu Leu Glu Leu Ile Arg Cys Asp Leu Glu Arg Ile Pro His Ser		
335	340	345
Ile Phe Ser Leu His Asn Leu Gln Glu Ile Asp Leu Lys Asp Asn		
350	355	360

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<210> 251
<211> 20
<212> DNA
<213> Artificial Sequence
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<223> Synthetic Oligonucleotide Probe

<400> 251  
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<210> 252  
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<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 252  
gatggctagg ttctggaggt tctg 24

<210> 253  
<211> 47  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 253  
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<210> 254  
<211> 1650  
<212> DNA  
<213> Homo Sapien

<400> 254  
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tgaacgcagg agctgtcatt gactggccca cagaggaggg caaggaagta 150  
tgggattatg tgacggtccg caaggatgcc tacatgttct ggtggctcta 200  
ttatgccacc aactcctgca agaacttctc agaactgccc ctggtcatgt 250  
ggttcaggg cggtccaggc ggttctagca ctggatttgg aaacttttag 300  
gaaattgggc cccttgacag tgatctcaa ccacggaaaa ccacctggct 350  
ccaggctgcc agtctcctat ttgtggataa tcccggtggc actgggttca 400  
gttatgtgaa tggtagtggt gcctatgcca aggacctggc tatggtggt 450  
tcagacatga tggttctcct gaagaccttc ttcaagtggc acaaagaatt 500  
ccagacagtt ccattctaca ttttctcaga gtcctatggc ggaaaaatgg 550  
cagctggcat tggtctagag ctttataagg ccattcagcg agggaccatc 600  
aagtgcact ttgcgggggt tgccttggt gattcctggc tctccccgt 650  
tgattcggtg ctctcctggg gaccttacct gtacagcatg tctcttcgt 700

aagacaaagg tctggcagag gtgtctaagg ttgcagagca agtactgaat 750  
 gccgtaaata aggggctcta cagagaggcc acagagctgt gggggaaagc 800  
 agaaatgatc attgaacaga acacagatgg ggtgaacttc tataacatct 850  
 taactaaaag cactcccacg tctacaatgg agtcgagtct agaattcaca 900  
 cagagccacc tagtttgtct ttgtcagcgc cacgtgagac acctacaacg 950  
 agatgcctta agccagctca tgaatggccc catcagaaag aagctaaaaa 1000  
 ttattcctga gnatcaatcc tggggaggcc aggctaccaa cgtcttg 1050  
 aacatggagg aggacttcat gaagccagtc attagcattg tggacgagtt 1100  
 gctggaggca gggatcaacg tgacggtgta taatggacag ctggatctca 1150  
 tcgtagatac catgggtcag gaggcctggg tgcggaaact gaagtggcca 1200  
 gaactgccta aattcagtca gctgaagtgg aaggccctgt acagtgaccc 1250  
 taaatcttg gaaacatctg ctttgcctaa gtcctacaag aacttgctt 1300  
 tctactggat tctgaaagct ggtcatatgg ttccttctga ccaaggggac 1350  
 atggctctga agatgatgag actggtgact cagcaagaat aggatggatg 1400  
 gggctggaga tgagctggtt tggccttggg gcacagagct gagctgaggc 1450  
 cgctgaagct gtaggaagcg ccattttcc ctgtatctaa ctggggctgt 1500  
 gatcaagaag gttctgacca gttctgcag aggataaaat cattgtctct 1550  
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 taaaaaaattg atttgttttgc atcaaaataa aggatgataa tagatattaa 1650

<210> 255  
<211> 452  
<212> PRT  
<213> Homo Sapien

<400> 255  
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 Leu Leu Pro Leu Leu Gly Leu Asn Ala Gly Ala Val Ile Asp  
 20 25 30  
 Trp Pro Thr Glu Glu Gly Lys Glu Val Trp Asp Tyr Val Thr Val  
 35 40 45

Arg Lys Asp Ala Tyr Met Phe Trp Trp Leu Tyr Tyr Ala Thr Asn  
 50 55 60  
 Ser Cys Lys Asn Phe Ser Glu Leu Pro Leu Val Met Trp Leu Gln  
 65 70 75  
 Gly Gly Pro Gly Gly Ser Ser Thr Gly Phe Gly Asn Phe Glu Glu  
 80 85 90  
 Ile Gly Pro Leu Asp Ser Asp Leu Lys Pro Arg Lys Thr Thr Trp  
 95 100 105  
 Leu Gln Ala Ala Ser Leu Leu Phe Val Asp Asn Pro Val Gly Thr  
 110 115 120  
 Gly Phe Ser Tyr Val Asn Gly Ser Gly Ala Tyr Ala Lys Asp Leu  
 125 130 135  
 Ala Met Val Ala Ser Asp Met Met Val Leu Leu Lys Thr Phe Phe  
 140 145 150  
 Ser Cys His Lys Glu Phe Gln Thr Val Pro Phe Tyr Ile Phe Ser  
 155 160 165  
 Glu Ser Tyr Gly Gly Lys Met Ala Ala Gly Ile Gly Leu Glu Leu  
 170 175 180  
 Tyr Lys Ala Ile Gln Arg Gly Thr Ile Lys Cys Asn Phe Ala Gly  
 185 190 195  
 Val Ala Leu Gly Asp Ser Trp Ile Ser Pro Val Asp Ser Val Leu  
 200 205 210  
 Ser Trp Gly Pro Tyr Leu Tyr Ser Met Ser Leu Leu Glu Asp Lys  
 215 220 225  
 Gly Leu Ala Glu Val Ser Lys Val Ala Glu Gln Val Leu Asn Ala  
 230 235 240  
 Val Asn Lys Gly Leu Tyr Arg Glu Ala Thr Glu Leu Trp Gly Lys  
 245 250 255  
 Ala Glu Met Ile Ile Glu Gln Asn Thr Asp Gly Val Asn Phe Tyr  
 260 265 270  
 Asn Ile Leu Thr Lys Ser Thr Pro Thr Ser Thr Met Glu Ser Ser  
 275 280 285  
 Leu Glu Phe Thr Gln Ser His Leu Val Cys Leu Cys Gln Arg His  
 290 295 300  
 Val Arg His Leu Gln Arg Asp Ala Leu Ser Gln Leu Met Asn Gly

305	310	315
Pro Ile Arg Lys Lys Leu Lys Ile Ile Pro Glu Asp Gln Ser Trp		
320	325	330
Gly Gly Gln Ala Thr Asn Val Phe Val Asn Met Glu Glu Asp Phe		
335	340	345
Met Lys Pro Val Ile Ser Ile Val Asp Glu Leu Leu Glu Ala Gly		
350	355	360
Ile Asn Val Thr Val Tyr Asn Gly Gln Leu Asp Leu Ile Val Asp		
365	370	375
Thr Met Gly Gln Glu Ala Trp Val Arg Lys Leu Lys Trp Pro Glu		
380	385	390
Leu Pro Lys Phe Ser Gln Leu Lys Trp Lys Ala Leu Tyr Ser Asp		
395	400	405
Pro Lys Ser Leu Glu Thr Ser Ala Phe Val Lys Ser Tyr Lys Asn		
410	415	420
Leu Ala Phe Tyr Trp Ile Leu Lys Ala Gly His Met Val Pro Ser		
425	430	435
Asp Gln Gly Asp Met Ala Leu Lys Met Met Arg Leu Val Thr Gln		
440	445	450

Gln Glu

<210> 256

<211> 1100

<212> DNA

<213> Homo Sapien

<400> 256

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tgctgctggc tcgggctgga ctcaggaagc cggagtgcga ggaggcggeg 100

ccgttatcag gaccatgcgg ccgacgggtc atcacgtcgc gcacgtggg 150

tggagaggac gccgaactcg ggcgttggcc gtggcagggg agcctgcgcc 200

tgtgggattc ccacgtatgc ggagtgagcc tgctcagcca ccgctggca 250

ctcacggcgg cgcaactgctt taaaacctat agtacaccaa gtatccctc 300

cgggtggatg gtccagtttgc cccagctgac ttccatgcca tccttctgga 350

gcctgcaggc ctactacacc cgttacttcg tatcgaatat ctatctgagc 400

cctcgctacc tggggattc accctatgac attgccttgg tgaagctgtc 450  
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 ccacatttga gtttgagaac cggacagact gctgggtgac tggctggggg 550  
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 tcaggtcgcc atcataaaca actctatgtg caaccacetc ttccctcaagt 650  
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 agtcaggccc tggttcttctt ctgtcttgg tggtaataaa cacattccag 1050  
 ttgatgcctt gcagggcatt cttaaaaaaa aaaaaaaaaa aaaaaaaaaa 1100

&lt;210&gt; 257

&lt;211&gt; 314

&lt;212&gt; PRT

&lt;213&gt; Homo Sapien

&lt;400&gt; 257

Met	Gly	Ala	Arg	Gly	Ala	Leu	Leu	Leu	Ala	Leu	Leu	Ala	Arg
1					5				10			15	

Ala	Gly	Leu	Arg	Lys	Pro	Glu	Ser	Gln	Glu	Ala	Ala	Pro	Leu	Ser
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

20		25		30										
----	--	----	--	----	--	--	--	--	--	--	--	--	--	--

Gly	Pro	Cys	Gly	Arg	Arg	Val	Ile	Thr	Ser	Arg	Ile	Val	Gly	Gly
35									40					45

Glu	Asp	Ala	Glu	Leu	Gly	Arg	Trp	Pro	Trp	Gln	Gly	Ser	Leu	Arg
50								55					60	

Leu	Trp	Asp	Ser	His	Val	Cys	Gly	Val	Ser	Leu	Leu	Ser	His	Arg
									65					75

Trp	Ala	Leu	Thr	Ala	Ala	His	Cys	Phe	Glu	Thr	Tyr	Ser	Asp	Leu
									80					90

Ser Asp Pro Ser Gly Trp Met Val Gln Phe Gly Gln Leu Thr Ser  
 95 100 105  
 Met Pro Ser Phe Trp Ser Leu Gln Ala Tyr Tyr Thr Arg Tyr Phe  
 110 115 120  
 Val Ser Asn Ile Tyr Leu Ser Pro Arg Tyr Leu Gly Asn Ser Pro  
 125 130 135  
 Tyr Asp Ile Ala Leu Val Lys Leu Ser Ala Pro Val Thr Tyr Thr  
 140 145 150  
 Lys His Ile Gln Pro Ile Cys Leu Gln Ala Ser Thr Phe Glu Phe  
 155 160 165  
 Glu Asn Arg Thr Asp Cys Trp Val Thr Gly Trp Gly Tyr Ile Lys  
 170 175 180  
 Glu Asp Glu Ala Leu Pro Ser Pro His Thr Leu Gln Glu Val Gln  
 185 190 195  
 Val Ala Ile Ile Asn Asn Ser Met Cys Asn His Leu Phe Leu Lys  
 200 205 210  
 Tyr Ser Phe Arg Lys Asp Ile Phe Gly Asp Met Val Cys Ala Gly  
 215 220 225  
 Asn Ala Gln Gly Gly Lys Asp Ala Cys Phe Gly Asp Ser Gly Gly  
 230 235 240  
 Pro Leu Ala Cys Asn Lys Asn Gly Leu Trp Tyr Gln Ile Gly Val  
 245 250 255  
 Val Ser Trp Gly Val Gly Cys Gly Arg Pro Asn Arg Pro Gly Val  
 260 265 270  
 Tyr Thr Asn Ile Ser His His Phe Glu Trp Ile Gln Lys Leu Met  
 275 280 285  
 Ala Gln Ser Gly Met Ser Gln Pro Asp Pro Ser Trp Pro Leu Leu  
 290 295 300  
 Phe Phe Pro Leu Leu Trp Ala Leu Pro Leu Leu Gly Pro Val  
 305 310  
 <210> 258  
 <211> 2427  
 <212> DNA  
 <213> Homo Sapien  
 <400> 258  
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cgagccccga ccagcggagg acgctgcccc caggctgggt gtcctgggc 150  
cgtcgccacc ctgaggaaga gctgagtctc acctttgccc tgagacagca 200  
gaatgtggaa agactctcg agctggtgca ggctgtgtcg gatcccagct 250  
ctcctcaata cgaaaatac ctgaccctag agaatgtggc tgatctggtg 300  
aggccatccc cactgaccct ccacacggtg caaaaatggc tcttggcagc 350  
cgagccccag aagtgccatt ctgtgatcac acaggacttt ctgacttgc 400  
ggctgagcat ccgacaagca gagctgctgc tccctggggc tgagttcat 450  
caactatgtgg gaggactac gaaaaacccat gtttaaggt ccccacatcc 500  
ctaccagctt ccacaggcct tggcccccata tgtggacttt gtggggggac 550  
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agtagccccgt gtgggtggac aacagggccg gggccggggcc gggattgagg 850  
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tgagctatgg agatgatgag gactccctca gcagcgccta catccagcgg 1050  
gtcaacactg agtcatgaa ggctgccgct cggggctca ccctgcttt 1100  
cgccctcaggt gacagtgggg cccgggtgtg gtctgtctct ggaagacacc 1150  
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 ctttacttag cttccaggc ttaacttctc tgactactct tgtcttcctc 2250  
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 tgttagttt tgctcttctc agtttactca ttgtccctg gaacaaatca 2350  
 ctgacatcta caaccattac catctacta aataagactt tctatccaaat 2400  
 aatgattgat acctcaaatg taaaaaa 2427

<210> 259  
 <211> 556  
 <212> PRT  
 <213> Homo Sapien

<400> 259  
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 1 5 10 15

Ser Gly Lys Cys Ser Tyr Ser Pro Glu Pro Asp Gln Arg Arg Thr

20	25	30
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35	40	45
Glu Leu Ser Leu Thr Phe Ala Leu Arg Gln Gln Asn Val Glu Arg		
50	55	60
Leu Ser Glu Leu Val Gln Ala Val Ser Asp Pro Ser Ser Pro Gln		
65	70	75
Tyr Gly Lys Tyr Leu Thr Leu Glu Asn Val Ala Asp Leu Val Arg		
80	85	90
Pro Ser Pro Leu Thr Leu His Thr Val Gln Lys Trp Leu Leu Ala		
95	100	105
Ala Gly Ala Gln Lys Cys His Ser Val Ile Thr Gln Asp Phe Leu		
110	115	120
Thr Cys Trp Leu Ser Ile Arg Gln Ala Glu Leu Leu Leu Pro Gly		
125	130	135
Ala Glu Phe His His Tyr Val Gly Gly Pro Thr Glu Thr His Val		
140	145	150
Val Arg Ser Pro His Pro Tyr Gln Leu Pro Gln Ala Leu Ala Pro		
155	160	165
His Val Asp Phe Val Gly Gly Leu His Arg Phe Pro Pro Thr Ser		
170	175	180
Ser Leu Arg Gln Arg Pro Glu Pro Gln Val Thr Gly Thr Val Gly		
185	190	195
Leu His Leu Gly Val Thr Pro Ser Val Ile Arg Lys Arg Tyr Asn		
200	205	210
Leu Thr Ser Gln Asp Val Gly Ser Gly Thr Ser Asn Asn Ser Gln		
215	220	225
Ala Cys Ala Gln Phe Leu Glu Gln Tyr Phe His Asp Ser Asp Leu		
230	235	240
Ala Gln Phe Met Arg Leu Phe Gly Gly Asn Phe Ala His Gln Ala		
245	250	255
Ser Val Ala Arg Val Val Gly Gln Gln Gly Arg Gly Arg Ala Gly		
260	265	270
Ile Glu Ala Ser Leu Asp Val Gln Tyr Leu Met Ser Ala Gly Ala		
275	280	285

Asn	Ile	Ser	Thr	Trp	Val	Tyr	Ser	Ser	Pro	Gly	Arg	His	Glu	Gly
				290			295					300		
Gln	Glu	Pro	Phe	Leu	Gln	Trp	Leu	Met	Leu	Leu	Ser	Asn	Glu	Ser
				305			310					315		
Ala	Leu	Pro	His	Val	His	Thr	Val	Ser	Tyr	Gly	Asp	Asp	Glu	Asp
				320			325					330		
Ser	Leu	Ser	Ser	Ala	Tyr	Ile	Gln	Arg	Val	Asn	Thr	Glu	Leu	Met
				335			340					345		
Lys	Ala	Ala	Ala	Arg	Gly	Leu	Thr	Leu	Leu	Phe	Ala	Ser	Gly	Asp
				350			355					360		
Ser	Gly	Ala	Gly	Cys	Trp	Ser	Val	Ser	Gly	Arg	His	Gln	Phe	Arg
				365			370					375		
Pro	Thr	Phe	Pro	Ala	Ser	Ser	Pro	Tyr	Val	Thr	Thr	Val	Gly	Gly
				380			385					390		
Thr	Ser	Phe	Gln	Glu	Pro	Phe	Leu	Ile	Thr	Asn	Glu	Ile	Val	Asp
				395			400					405		
Tyr	Ile	Ser	Gly	Gly	Phe	Ser	Asn	Val	Phe	Pro	Arg	Pro	Ser	
				410			415					420		
Tyr	Gln	Glu	Glu	Ala	Val	Thr	Lys	Phe	Leu	Ser	Ser	Ser	Pro	His
				425			430					435		
Leu	Pro	Pro	Ser	Ser	Tyr	Phe	Asn	Ala	Ser	Gly	Arg	Ala	Tyr	Pro
				440			445					450		
Asp	Val	Ala	Ala	Leu	Ser	Asp	Gly	Tyr	Trp	Val	Val	Ser	Asn	Arg
				455			460					465		
Val	Pro	Ile	Pro	Trp	Val	Ser	Gly	Thr	Ser	Ala	Ser	Thr	Pro	Val
				470			475					480		
Phe	Gly	Gly	Ile	Leu	Ser	Leu	Ile	Asn	Glu	His	Arg	Ile	Leu	Ser
				485			490					495		
Gly	Arg	Pro	Pro	Leu	Gly	Phe	Leu	Asn	Pro	Arg	Leu	Tyr	Gln	Gln
				500			505					510		
His	Gly	Ala	Gly	Leu	Phe	Asp	Val	Thr	Arg	Gly	Cys	His	Glu	Ser
				515			520					525		
Cys	Leu	Asp	Glu	Glu	Val	Glu	Gly	Gln	Gly	Phe	Cys	Ser	Gly	Pro
				530			535					540		
Gly	Trp	Asp	Pro	Val	Thr	Gly	Trp	Gly	Thr	Pro	Thr	Ser	Gln	Leu
				545			550					555		

## Cys

<210> 260  
<211> 1638  
<212> DNA  
<213> Homo Sapien

<400> 260  
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cgccggccgg gccccgtgt cggcgccgaa cagtgtcg 100  
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agtggccct tacagtgc 200  
cctggaaacc cacttggcct gcataccgcc 250  
tccctgtcgt cttgccccag tctaccctca atttagccaa gccagactt 300  
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taagggact ccactgccc 400  
cttacgaaga gccaagcaa tatctgtctt 450  
atgaaacgct ctatgcaat ggcagccgca cagagacgca ggtgggcattc 500  
tacatcctca gcagtagtgg agatggggcc caacaccgag actcagggtc 550  
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tcagcatttt tgggaaggac ttctgtc 650  
actaccctt ctaaacatca 650  
gtgaagttat ccacgggctg caccggcacc ctgggtggcag agaagcatgt 700  
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 tgactggctt tactatttga aaactggttt gtgtatcata tcataatatca 1450  
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 tttggggcaa tgaggaatat ttgacaatta agtaatctt cacgttttg 1550  
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 atattggca tacaagagat atgaaaaaaaaaaaaaaa 1638

<210> 261  
 <211> 383  
 <212> PRT  
 <213> Homo Sapien

<400> 261  
 Met Ala Gly Ile Pro Gly Leu Leu Phe Leu Leu Phe Phe Leu Leu  
 1 5 10 15  
 Cys Ala Val Gly Gln Val Ser Pro Tyr Ser Ala Pro Trp Lys Pro  
 20 25 30  
 Thr Trp Pro Ala Tyr Arg Leu Pro Val Val Leu Pro Gln Ser Thr  
 35 40 45  
 Leu Asn Leu Ala Lys Pro Asp Phe Gly Ala Glu Ala Lys Leu Glu  
 50 55 60  
 Val Ser Ser Ser Cys Gly Pro Gln Cys His Lys Gly Thr Pro Leu  
 65 70 75  
 Pro Thr Tyr Glu Glu Ala Lys Gln Tyr Leu Ser Tyr Glu Thr Leu  
 80 85 90  
 Tyr Ala Asn Gly Ser Arg Thr Glu Thr Gln Val Gly Ile Tyr Ile  
 95 100 105  
 Leu Ser Ser Ser Gly Asp Gly Ala Gln His Arg Asp Ser Gly Ser  
 110 115 120

Ser Gly Lys Ser Arg Arg Lys Arg Gln Ile Tyr Gly Tyr Asp Ser  
 125 130 135  
 Arg Phe Ser Ile Phe Gly Lys Asp Phe Leu Leu Asn Tyr Pro Phe  
 140 145 150  
 Ser Thr Ser Val Lys Leu Ser Thr Gly Cys Thr Gly Thr Leu Val  
 155 160 165  
 Ala Glu Lys His Val Leu Thr Ala Ala His Cys Ile His Asp Gly  
 170 175 180  
 Lys Thr Tyr Val Lys Gly Thr Gln Lys Leu Arg Val Gly Phe Leu  
 185 190 195  
 Lys Pro Lys Phe Lys Asp Gly Gly Arg Gly Ala Asn Asp Ser Thr  
 200 205 210  
 Ser Ala Met Pro Glu Gln Met Lys Phe Gln Trp Ile Arg Val Lys  
 215 220 225  
 Arg Thr His Val Pro Lys Gly Trp Ile Lys Gly Asn Ala Asn Asp  
 230 235 240  
 Ile Gly Met Asp Tyr Asp Tyr Ala Leu Leu Glu Leu Lys Lys Pro  
 245 250 255  
 His Lys Arg Lys Phe Met Lys Ile Gly Val Ser Pro Pro Ala Lys  
 260 265 270  
 Gln Leu Pro Gly Gly Arg Ile His Phe Ser Gly Tyr Asp Asn Asp  
 275 280 285  
 Arg Pro Gly Asn Leu Val Tyr Arg Phe Cys Asp Val Lys Asp Glu  
 290 295 300  
 Thr Tyr Asp Leu Leu Tyr Gln Gln Cys Asp Ala Gln Pro Gly Ala  
 305 310 315  
 Ser Gly Ser Gly Val Tyr Val Arg Met Trp Lys Arg Gln Gln Gln  
 320 325 330  
 Lys Trp Glu Arg Lys Ile Ile Gly Ile Phe Ser Gly His Gln Trp  
 335 340 345  
 Val Asp Met Asn Gly Ser Pro Gln Asp Phe Asn Val Ala Val Arg  
 350 355 360  
 Ile Thr Pro Leu Lys Tyr Ala Gln Ile Cys Tyr Trp Ile Lys Gly  
 365 370 375  
 Asn Tyr Leu Asp Cys Arg Glu Gly  
 380

<210> 262  
<211> 1378  
<212> DNA  
<213> Homo Sapien

<400> 262  
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acottcacct ccctgctgct gctggcgctg acagccatcc tcaatgcggc 150  
caggataacct gttcccccag cctgtggaa gccccagcag ctgaaccggg 200  
tttgtggcgg cgaggacagc actgacagcg agtggccctg gatcgtgagc 250  
atccagaaga atgggaccca ccactgcgca ggttctctgc tcaccagccg 300  
ctgggtgatc actgctgecc actgtttcaa ggacaacctg aacaaaccat 350  
acctgttctc tgtgctgctg ggggcctggc agctggggaa ccctggctct 400  
cggtcccaga aggtgggtgt tgccctgggtg gagccccacc ctgtgtattc 450  
ctggaaggaa ggtgcctgtg cagacattgc cctggtgctg ctcgagcgct 500  
ccatacagtt ctcagagcgg gtcctgccc tctgcctacc tgatgcctct 550  
atccacactcc ctccaaacac ccactgctgg atctcaggct gggggagcat 600  
ccaagatgga gttcccttgc cccaccctca gaccctgcag aagctgaagg 650  
ttcctatcat cgactcggaa gtctgcagcc atctgtactg gggggagaca 700  
ggacagggac ccatcactga ggacatgctg tgtgccggct acttggaggg 750  
ggagcgggat gcttgtctgg gcgactccgg gggccccctc atgtgccagg 800  
tggacggcgc ctggctgctg gccggcatca tcagctgggg cgaggcgtgt 850  
gccgagcgca acaggccccgg ggtctacatc agcctctctg cgcaccgctc 900  
ctgggtggag aagatcgtgc aagggttgca gtcggcgccc cgcgctcagg 950  
gggggtggggc cctcaggcga ccgagccagg gctctggggc cgccgcgcgc 1000  
tccttagggcg cagcgggacg cggggctcgg atctgaaagg cggccagatc 1050  
cacatctgga tctggatctg cggcggcctc gggcggttc ccccgccgta 1100  
aataggctca tctacactcta cctctggggg cccggacggc tgctgcggaa 1150

agaaaaacccc ctccccgacc cgcccgacgg cctcaggccc ccctccaagg 1200  
 catcaggccc cgcccaacgg cctcatgtcc ccgcccccac gacttccggc 1250  
 cccgcggccg ggccccagcg ctttgtgtataataatgtt aatgattttt 1300  
 ataggtattt gtaaccctgc ccacatatct tatttattcc tccaatttca 1350  
 ataaattatt tattctccaa aaaaaaaaa 1378

&lt;210&gt; 263

&lt;211&gt; 317

&lt;212&gt; PRT

&lt;213&gt; Homo Sapien.

&lt;400&gt; 263

Met	Val	Val	Ser	Gly	Ala	Pro	Pro	Ala	Leu	Gly	Gly	Gly	Cys	Leu
1					5				10					15
Gly	Thr	Phe	Thr	Ser	Leu	Leu	Leu	Leu	Ala	Ser	Thr	Ala	Ile	Leu
					20				25					30
Asn	Ala	Ala	Arg	Ile	Pro	Val	Pro	Pro	Ala	Cys	Gly	Lys	Pro	Gln
					35				40					45
Gln	Leu	Asn	Arg	Val	Val	Gly	Gly	Glu	Asp	Ser	Thr	Asp	Ser	Glu
					50			55						60
Trp	Pro	Trp	Ile	Val	Ser	Ile	Gln	Lys	Asn	Gly	Thr	His	His	Cys
					65				70					75
Ala	Gly	Ser	Leu	Leu	Thr	Ser	Arg	Trp	Val	Ile	Thr	Ala	Ala	His
					80				85					90
Cys	Phe	Lys	Asp	Asn	Leu	Asn	Lys	Pro	Tyr	Leu	Phe	Ser	Val	Leu
					95			100						105
Leu	Gly	Ala	Trp	Gln	Leu	Gly	Asn	Pro	Gly	Ser	Arg	Ser	Gln	Lys
					110				115					120
Val	Gly	Val	Ala	Trp	Val	Glu	Pro	His	Pro	Val	Tyr	Ser	Trp	Lys
					125				130					135
Glu	Gly	Ala	Cys	Ala	Asp	Ile	Ala	Leu	Val	Arg	Leu	Glu	Arg	Ser
					140				145					150
Ile	Gln	Phe	Ser	Glu	Arg	Val	Leu	Pro	Ile	Cys	Leu	Pro	Asp	Ala
					155				160					165
Ser	Ile	His	Leu	Pro	Pro	Asn	Thr	His	Cys	Trp	Ile	Ser	Gly	Trp
					170				175					180

Gly Ser Ile Gln Asp Gly Val Pro Leu Pro His Pro Gln Thr Leu  
 185 190 195  
 Gln Lys Leu Lys Val Pro Ile Ile Asp Ser Glu Val Cys Ser His  
 200 205 210  
 Leu Tyr Trp Arg Gly Ala Gly Gln Gly Pro Ile Thr Glu Asp Met  
 215 220 225  
 Leu Cys Ala Gly Tyr Leu Glu Gly Glu Arg Asp Ala Cys Leu Gly  
 230 235 240  
 Asp Ser Gly Gly Pro Leu Met Cys Gln Val Asp Gly Ala Trp Leu  
 245 250 255  
 Leu Ala Gly Ile Ile Ser Trp Gly Glu Gly Cys Ala Glu Arg Asn  
 260 265 270  
 Arg Pro Gly Val Tyr Ile Ser Leu Ser Ala His Arg Ser Trp Val  
 275 280 285  
 Glu Lys Ile Val Gln Gly Val Gln Leu Arg Gly Arg Ala Gln Gly  
 290 295 300  
 Gly Gly Ala Leu Arg Ala Pro Ser Gln Gly Ser Gly Ala Ala Ala  
 305 310 315

Arg Ser

<210> 264  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic Oligonucleotide Probe

<400> 264  
gtccgcaagg atgcctacat gttc 24

<210> 265  
 <211> 19  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic Oligonucleotide Probe

<400> 265  
gcagaggtgt ctaaggttg 19

<210> 266  
 <211> 24

<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 266  
agctctagac caatgccagc ttcc 24

<210> 267  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 267  
gccaccaact cctgcaagaa cttctcagaa ctgcccctgg tcatg 45

<210> 268  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 268  
gggaaattca ccctatgaca ttgcc 25

<210> 269  
<211> 24  
<212> DNA  
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<220>  
<223> Synthetic Oligonucleotide Probe

<400> 269  
gaatgccctg caagcatcaa ctgg 24

<210> 270  
<211> 50  
<212> DNA  
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<220>  
<223> Synthetic Oligonucleotide Probe

<400> 270  
gcacctgtca cctacactaa acacatccag cccatctgtc tccaggcctc 50

<210> 271  
<211> 26  
<212> DNA  
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<220>  
<223> Synthetic Oligonucleotide Probe

<400> 271  
gcggaagggc agaatggac tccaaag 26

<210> 272  
<211> 18  
<212> DNA  
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<220>  
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<400> 272  
cagccctgcc acatgtgc 18

<210> 273  
<211> 18  
<212> DNA  
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<220>  
<223> Synthetic Oligonucleotide Probe

<400> 273  
tactgggtgg tcagcaac 18

<210> 274  
<211> 24  
<212> DNA  
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<220>  
<223> Synthetic Oligonucleotide Probe

<400> 274  
ggcgaagagc agggtgagac cccg 24

<210> 275  
<211> 45

<212> DNA  
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<220>  
<223> Synthetic Oligonucleotide Probe

<400> 275  
gcctcatcc tctctggcaa atgcagttac agcccgagc ccgac 45

<210> 276

<211> 21

<212> DNA

<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 276  
ggcaggat tccagggttc c 21

<210> 277

<211> 18

<212> DNA

<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 277  
ggctatgaca gcaggttc 18

<210> 278

<211> 18

<212> DNA

<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 278  
tgacaatgac cgaccagg 18

<210> 279

<211> 24

<212> DNA

<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 279  
gcatcgatt gctggtagag caag 24

<210> 280

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 280  
ttacagtgcc ccctggaaac ccacttggcc tgcataaccgc ctccc 45

<210> 281

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 281

cgtctcgagc gctccataca gttcccttgc ccca 34

<210> 282

<211> 61

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 282

tggaggggga gcgggatgct tgtctggcg actccggggg cccccctcatg 50

tgccaggtgg a 61

<210> 283

<211> 119

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 283

ccctcagacc ctgcagaagc tgaaggttcc tatcatcgac tcggaagtct 50

gcagccatct gtactggcgg ggagcaggac agggacccat cactgaggac 100

atgctgtgtg ccggctact 119

<210> 284

<211> 1875

<212> DNA

<213> Homo Sapien

<400> 284

gacggctggc caccatgcac ggctcctgca gtttcctgat gcttctgctg 50

ccgctactgc tactgctggt ggccaccaca ggccccgttg gagccctcac 100

agatgaggag aaacgttga tggtagct gcacaacctc taccggccc 150  
aggatatcccc gacggcctca gacatgctgc acatgagatg ggacgaggag 200  
ctggccgcct tcgccaaggc ctacgcacgg cagtgcgtgt ggggccacaa 250  
caaggagcgc gggcgccgcg gcgagaatct gttcgccatc acagacgagg 300  
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caaggcttagc gttgtgtcag ggctgaactc gggccctggc catgtgtggg 1350  
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tgcccacaca gcatgtgcgc tctccctgag tgccctgtgt a gctggggatg 1750  
gggattccta ggggcagatg aaggacaagc cccactggag tggggttctt 1800  
tgagtggggg aggcaaggac gagggaaagga aagtaactcc tgactctcca 1850  
ataaaaaacct gtccaaacctg tgaaa 1875

<210> 285

<211> 463

<212> PRT

<213> Homo Sapien

<400> 285

Met His Gly Ser Cys Ser Phe Leu Met Leu Leu Leu Pro Ile Leu  
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Glu Glu Lys Arg Leu Met Val Glu Leu His Asn Leu Tyr Arg Ala  
35 40 45

Glu Glu Leu Ala Ala Phe Ala Lys Ala Tyr Ala Arg Gln Cys Val  
65 70 75

Trp Gly His Asn Lys Glu Arg Gly Arg Arg Gly Glu Asn Leu Phe  
                   80                  85                                 90

Ala Ile Thr Asp Glu Gly Met Asp Val Pro Leu Ala Met Glu Glu  
95 100 105

Ser Pro Gly Gln Met Cys Gly His Tyr Thr Gln Val Val Trp Ala  
125 130 135

Lys Thr Glu Arg Ile Gly Cys Gly Ser His Phe Cys Glu Lys Leu  
 140 145 150  
 Gln Gly Val Glu Glu Thr Asn Ile Glu Leu Leu Val Cys Asn Tyr  
 155 160 165  
 Glu Pro Pro Gly Asn Val Lys Gly Lys Arg Pro Tyr Gln Glu Gly  
 170 175 180  
 Thr Pro Cys Ser Gln Cys Pro Ser Gly Tyr His Cys Lys Asn Ser  
 185 190 195  
 Leu Cys Glu Pro Ile Gly Ser Pro Glu Asp Ala Gln Asp Leu Pro  
 200 205 210  
 Tyr Leu Val Thr Glu Ala Pro Ser Phe Arg Ala Thr Glu Ala Ser  
 215 220 225  
 Asp Ser Arg Lys Met Gly Thr Pro Ser Ser Leu Ala Thr Gly Ile  
 230 235 240  
 Pro Ala Phe Leu Val Thr Glu Val Ser Gly Ser Leu Ala Thr Lys  
 245 250 255  
 Ala Leu Pro Ala Val Glu Thr Gln Ala Pro Thr Ser Leu Ala Thr  
 260 265 270  
 Lys Asp Pro Pro Ser Met Ala Thr Glu Ala Pro Pro Cys Val Thr  
 275 280 285  
 Thr Glu Val Pro Ser Ile Leu Ala Ala His Ser Leu Pro Ser Leu  
 290 295 300  
 Asp Glu Glu Pro Val Thr Phe Pro Lys Ser Thr His Val Pro Ile  
 305 310 315  
 Pro Lys Ser Ala Asp Lys Val Thr Asp Lys Thr Lys Val Pro Ser  
 320 325 330  
 Arg Ser Pro Glu Asn Ser Leu Asp Pro Lys Met Ser Leu Thr Gly  
 335 340 345  
 Ala Arg Glu Leu Leu Pro His Ala Gln Glu Glu Ala Glu Ala Glu  
 350 355 360  
 Ala Glu Leu Pro Pro Ser Ser Glu Val Leu Ala Ser Val Phe Pro  
 365 370 375  
 Ala Gln Asp Lys Pro Gly Glu Leu Gln Ala Thr Leu Asp His Thr  
 380 385 390  
 Gly His Thr Ser Ser Lys Ser Leu Pro Asn Phe Pro Asn Thr Ser  
 395 400 405

Ala Thr Ala Asn Ala Thr Gly Gly Arg Ala Leu Ala Leu Gln Ser  
410 415 420  
Ser Leu Pro Gly Ala Glu Gly Pro Asp Lys Pro Ser Val Val Ser  
425 430 435  
Gly Leu Asn Ser Gly Pro Gly His Val Trp Gly Pro Leu Leu Gly  
440 445 450  
Leu Leu Leu Leu Pro Pro Leu Val Leu Ala Gly Ile Phe  
455 460

<210> 286

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 286

tcctgcagtt tcctgatgc 19

<210> 287

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 287

ctcatattgc acaccagtaa ttcg 24

<210> 288

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 288

atgaggagaa acgtttgatg gtggagctgc acaacctcta ccggg 45

<210> 289

<211> 3662

<212> DNA

<213> Homo Sapien

<400> 289

gtaactgaag tcaggcttt catttggaa gccccctcaa cagaattcgg 50

tcattctcca agttatggtg gacgtacttc tgggttctc cctctgctt 100  
cttttcaca ttagcagacc ggacttaagt cacaacagat tatctttcat 150  
caaggcaagt tccatgagcc accttcaaag cttcgagaa gtgaaactga 200  
acaacaatga attggagacc attccaaatc tgggaccagt ctggcaaat 250  
attacacttc tctccttggc tgaaaacagg attgttggaa tactccctga 300  
acatctgaaa gagttcagt ccctgaaac tttggacctt agcagcaaca 350  
atatttcaga gctccaaact gcatttccag ccctacagct caaatatctg 400  
tatctcaaca gcaaccgagt cacatcaatg gaacctgggt attttgacaa 450  
tttggccaac acactccttg tggtaaagct gaacaggaac cgaatctcag 500  
ctatcccacc caagatgttt aaactgcccc aactgcaaca tctcgaattg 550  
aaccgaaaca agattaaaaa tggatggaa ctgacattcc aaggccttgg 600  
tgctctgaag tctctgaaaa tggatggaaa tggagtaacg aaacttatgg 650  
atggagctt ttggggctg agcaacatgg aaatttgca gctggaccat 700  
aacaacctaa cagagattac caaaggctgg cttaacggct tgctgatgct 750  
gcaggaactt catctcagcc aaaatgccat caacaggatc agccctgatg 800  
cctggagtt ctgccagaag ctcagtgagc tggacctaac tttcaatcac 850  
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cacagtgggt ggcggaaaac aacttcaga gctttgtaaa tgccagttgt 1300  
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tggctttgtg tgtgatgatt ttcccaaacc ccagatcacg gttcagccag 1400  
aaacacagtc ggcaataaaaa ggttccaatt tgagttcat ctgctcagct 1450  
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actactgcat gatgctgaaa tggaaaatta tgcacacctc cgggcccaga 1550  
gtggcgaggt gatggagtat accaccatcc ttcggctgct cgagggtggaa 1600  
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 <212> PRT  
 <213> Homo Sapien

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Ala Ser Ser Met Ser His Leu Gln Ser Leu Arg Glu Val Lys Leu  
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 Asn Asn Asn Glu Leu Glu Thr Ile Pro Asn Leu Gly Pro Val Ser  
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 Ala Asn Ile Thr Leu Leu Ser Leu Ala Gly Asn Arg Ile Val Glu  
                   65                        70                        75  
  
 Ile Leu Pro Glu His Leu Lys Glu Phe Gln Ser Leu Glu Thr Leu  
                   80                        85                        90  
  
 Asp Leu Ser Ser Asn Asn Ile Ser Glu Leu Gln Thr Ala Phe Pro  
                   95                        100                      105  
  
 Ala Leu Gln Leu Lys Tyr Leu Tyr Leu Asn Ser Asn Arg Val Thr  
                   110                      115                      120  
  
 Ser Met Glu Pro Gly Tyr Phe Asp Asn Leu Ala Asn Thr Leu Leu  
                   125                      130                      135  
  
 Val Leu Lys Leu Asn Arg Asn Arg Ile Ser Ala Ile Pro Pro Lys  
                   140                      145                      150  
  
 Met Phe Lys Leu Pro Gln Leu Gln His Leu Glu Leu Asn Arg Asn  
                   155                      160                      165  
  
 Lys Ile Lys Asn Val Asp Gly Leu Thr Phe Gln Gly Leu Gly Ala  
                   170                      175                      180  
  
 Leu Lys Ser Leu Lys Met Gln Arg Asn Gly Val Thr Lys Leu Met  
                   185                      190                      195  
  
 Asp Gly Ala Phe Trp Gly Leu Ser Asn Met Glu Ile Leu Gln Leu  
                   200                      205                      210  
  
 Asp His Asn Asn Leu Thr Glu Ile Thr Lys Gly Trp Leu Tyr Gly  
                   215                      220                      225  
  
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 Arg Ile Ser Pro Asp Ala Trp Glu Phe Cys Gln Lys Leu Ser Glu  
                   245                      250                      255  
  
 Leu Asp Leu Thr Phe Asn His Leu Ser Arg Leu Asp Asp Ser Ser  
                   260                      265                      270  
  
 Phe Leu Gly Leu Ser Leu Leu Asn Thr Leu His Ile Gly Asn Asn  
                   275                      280                      285  
  
 Arg Val Ser Tyr Ile Ala Asp Cys Ala Phe Arg Gly Leu Ser Ser

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Glu Asp Met Asn Gly Ala Phe Ser Gly Leu Asp Lys Leu Arg Arg		
320	325	330
Leu Ile Leu Gln Gly Asn Arg Ile Arg Ser Ile Thr Lys Lys Ala		
335	340	345
Phe Thr Gly Leu Asp Ala Leu Glu His Leu Asp Leu Ser Asp Asn		
350	355	360
Ala Ile Met Ser Leu Gln Gly Asn Ala Phe Ser Gln Met Lys Lys		
365	370	375
Leu Gln Gln Leu His Leu Asn Thr Ser Ser Leu Leu Cys Asp Cys		
380	385	390
Gln Leu Lys Trp Leu Pro Gln Trp Val Ala Glu Asn Asn Phe Gln		
395	400	405
Ser Phe Val Asn Ala Ser Cys Ala His Pro Gln Leu Leu Lys Gly		
410	415	420
Arg Ser Ile Phe Ala Val Ser Pro Asp Gly Phe Val Cys Asp Asp		
425	430	435
Phe Pro Lys Pro Gln Ile Thr Val Gln Pro Glu Thr Gln Ser Ala		
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Ile Lys Gly Ser Asn Leu Ser Phe Ile Cys Ser Ala Ala Ser Ser		
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Ser Asp Ser Pro Met Thr Phe Ala Trp Lys Lys Asp Asn Glu Leu		
470	475	480
Leu His Asp Ala Glu Met Glu Asn Tyr Ala His Leu Arg Ala Gln		
485	490	495
Gly Gly Glu Val Met Glu Tyr Thr Thr Ile Leu Arg Leu Arg Glu		
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Val Glu Phe Ala Ser Glu Gly Lys Tyr Gln Cys Val Ile Ser Asn		
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His Phe Gly Ser Ser Tyr Ser Val Lys Ala Lys Leu Thr Val Asn		
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Met Leu Pro Ser Phe Thr Lys Thr Pro Met Asp Leu Thr Ile Arg		
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 Phe Phe Ile Val Asp Val Lys Ile Glu Asp Ile Gly Val Tyr Ser  
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 Cys Thr Ala Gln Asn Ser Ala Gly Ser Ile Ser Ala Asn Ala Thr  
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 Arg Thr Val Thr Lys Gly Glu Thr Ala Val Leu Gln Cys Ile Ala  
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 Gly Gly Ser Pro Pro Pro Lys Leu Asn Trp Thr Lys Asp Asp Ser  
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 Pro Leu Val Val Thr Glu Arg His Phe Phe Ala Ala Gly Asn Gln  
 680 685 690  
 Leu Leu Ile Ile Val Asp Ser Asp Val Ser Asp Ala Gly Lys Tyr  
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 Thr Cys Glu Met Ser Asn Thr Leu Gly Thr Glu Arg Gly Asn Val  
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 Arg Leu Ser Val Ile Pro Thr Pro Thr Cys Asp Ser Pro Gln Met  
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 Thr Ala Pro Ser Leu Asp Asp Asp Gly Trp Ala Thr Val Gly Val  
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 Val Ile Ile Ala Val Val Cys Cys Val Val Gly Thr Ser Leu Val  
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 Trp Val Val Ile Ile Tyr His Thr Arg Arg Arg Asn Glu Asp Cys  
 770 775 780  
 Ser Ile Thr Asn Thr Asp Glu Thr Asn Leu Pro Ala Asp Ile Pro  
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 Ser Tyr Leu Ser Ser Gln Gly Thr Leu Ala Asp Arg Gln Asp Gly  
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Tyr Val Ser Ser Glu Ser Gly Ser His His Gln Phe Val Thr Ser  
 815 820 825  
 Ser Gly Ala Gly Phe Phe Leu Pro Gln His Asp Ser Ser Gly Thr  
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 Cys His Ile Asp Asn Ser Ser Glu Ala Asp Val Glu Ala Ala Thr  
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 Asp Leu Phe Leu Cys Pro Phe Leu Gly Ser Thr Gly Pro Met Tyr  
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 Leu Lys Gly Asn Val Tyr Gly Ser Asp Pro Phe Glu Thr Tyr His  
 875 880 885  
 Thr Gly Cys Ser Pro Asp Pro Arg Thr Val Leu Met Asp His Tyr  
 890 895 900  
 Glu Pro Ser Tyr Ile Lys Lys Lys Glu Cys Tyr Pro Cys Ser His  
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 Pro Ser Glu Glu Ser Cys Glu Arg Ser Phe Ser Asn Ile Ser Trp  
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 Pro Ser His Val Arg Lys Leu Leu Asn Thr Ser Tyr Ser His Asn  
 935 940 945  
 Glu Gly Pro Gly Met Lys Asn Leu Cys Leu Asn Lys Ser Ser Leu  
 950 955 960  
 Asp Phe Ser Ala Asn Pro Glu Pro Ala Ser Val Ala Ser Ser Asn  
 965 970 975  
 Ser Phe Met Gly Thr Phe Gly Lys Ala Leu Arg Arg Pro His Leu  
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 Asp Ala Tyr Ser Ser Phe Gly Gln Pro Ser Asp Cys Gln Pro Arg  
 995 1000 1005  
 Ala Phe Tyr Leu Lys Ala His Ser Ser Pro Asp Leu Asp Ser Gly  
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 Ser Glu Glu Asp Gly Lys Glu Arg Thr Asp Phe Gln Glu Glu Asn  
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&lt;212&gt; DNA

&lt;213&gt; Homo Sapien

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<211> 640

<212> PRT

<213> Homo Sapien

<400> 292

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Leu Ala Leu Gln Leu Leu Val Val Ala Gly Leu Val Arg Ala Gln  
35 40 45

Thr Cys Pro Ser Val Cys Ser Cys Ser Asn Gln Phe Ser Lys Val  
50 55 60

Ile Cys Val Arg Lys Asn Leu Arg Glu Val Pro Asp Gly Ile Ser  
65 70 75

Thr Asn Thr Arg Leu Leu Asn Leu His Glu Asn Gln Ile Gln Ile  
80 85 90

Ile Lys Val Asn Ser Phe Lys His Leu Arg His Leu Glu Ile Leu  
      65                 100                 105

Gln Leu Ser Arg Asn His Ile Arg Thr Ile Glu Ile Gly Ala Phe  
100 110 115 120

Asn Gly Leu Ala Asn Leu Asn Thr Leu Glu Leu Phe Asp Asn Arg  
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Leu Thr Thr Ile Pro Asn Gly Ala Phe Val Tyr Leu Ser Lys Leu  
145 150

Ile Glu Ile Trp Ile Arg Asn Asn Pro Ile Glu Ser Ile Pro Ser

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170	175	180
Glu Leu Lys Arg Leu Ser Tyr Ile Ser Glu Gly Ala Phe Glu Gly		
185	190	195
Leu Ser Asn Leu Arg Tyr Leu Asn Leu Ala Met Cys Asn Leu Arg		
200	205	210
Glu Ile Pro Asn Leu Thr Pro Leu Ile Lys Leu Asp Glu Leu Asp		
215	220	225
Leu Ser Gly Asn His Leu Ser Ala Ile Arg Pro Gly Ser Phe Gln		
230	235	240
Gly Leu Met His Leu Gln Lys Leu Trp Met Ile Gln Ser Gln Ile		
245	250	255
Gln Val Ile Glu Arg Asn Ala Phe Asp Asn Leu Gln Ser Leu Val		
260	265	270
Glu Ile Asn Leu Ala His Asn Asn Leu Thr Leu Leu Pro His Asp		
275	280	285
Leu Phe Thr Pro Leu His His Leu Glu Arg Ile His Leu His His		
290	295	300
Asn Pro Trp Asn Cys Asn Cys Asp Ile Leu Trp Leu Ser Trp Trp		
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Ile Lys Asp Met Ala Pro Ser Asn Thr Ala Cys Cys Ala Arg Cys		
320	325	330
Asn Thr Pro Pro Asn Leu Lys Gly Arg Tyr Ile Gly Glu Leu Asp		
335	340	345
Gln Asn Tyr Phe Thr Cys Tyr Ala Pro Val Ile Val Glu Pro Pro		
350	355	360
Ala Asp Leu Asn Val Thr Glu Gly Met Ala Ala Glu Leu Lys Cys		
365	370	375
Arg Ala Ser Thr Ser Leu Thr Ser Val Ser Trp Ile Thr Pro Asn		
380	385	390
Gly Thr Val Met Thr His Gly Ala Tyr Lys Val Arg Ile Ala Val		
395	400	405
Leu Ser Asp Gly Thr Leu Asn Phe Thr Asn Val Thr Val Gln Asp		
410	415	420

Thr Gly Met Tyr Thr Cys Met Val Ser Asn Ser Val Gly Asn Thr  
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 Thr Ala Ser Ala Thr Leu Asn Val Thr Ala Ala Thr Thr Thr Pro  
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 Phe Ser Tyr Phe Ser Thr Val Thr Val Glu Thr Met Glu Pro Ser  
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 Asp Ile Asn Ser Gly Ile Pro Gly Ile Asp Glu Val Met Lys Thr  
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 Thr Lys Ile Ile Ile Gly Cys Phe Val Ala Ile Thr Leu Met Ala  
 530 535 540  
 Ala Val Met Leu Val Ile Phe Tyr Lys Met Arg Lys Gln His His  
 545 550 555  
 Arg Gln Asn His His Ala Pro Thr Arg Thr Val Glu Ile Ile Asn  
 560 565 570  
 Val Asp Asp Glu Ile Thr Gly Asp Thr Pro Met Glu Ser His Leu  
 575 580 585  
 Pro Met Pro Ala Ile Glu His Glu His Leu Asn His Tyr Asn Ser  
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 Tyr Lys Ser Pro Phe Asn His Thr Thr Thr Val Asn Thr Ile Asn  
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<211> 1119

<212> PRT

<213> Homo Sapien

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Gly	Arg	Gly	Glu	Leu	Gly	Gln	Pro	Ser	Gly	Val	Ala	Ala	Glu	Arg
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Pro	Cys	Pro	Thr	Thr	Cys	Arg	Cys	Leu	Gly	Asp	Leu	Leu	Asp	Cys
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Val	Ala	Arg	Leu	Asp	Leu	Ser	His	Asn	Arg	Leu	Ser	Phe	Ile	Lys
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Ile	Leu	Pro	Glu	His	Leu	Lys	Glu	Phe	Gln	Ser	Leu	Glu	Thr	Leu
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Ser	Met	Glu	Pro	Gly	Tyr	Phe	Asp	Asn	Leu	Ala	Asn	Thr	Leu	Leu
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Val	Leu	Lys	Leu	Asn	Arg	Asn	Arg	Ile	Ser	Ala	Ile	Pro	Pro	Lys
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Asp Gly Ala Phe Trp Gly Leu Ser Asn Met Glu Ile Leu Gln Leu		
260	265	270
Asp His Asn Asn Leu Thr Glu Ile Thr Lys Gly Trp Leu Tyr Gly		
275	280	285
Leu Leu Met Leu Gln Glu Leu His Leu Ser Gln Asn Ala Ile Asn		
290	295	300
Arg Ile Ser Pro Asp Ala Trp Glu Phe Cys Gln Lys Leu Ser Glu		
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Phe Leu Gly Leu Ser Leu Leu Asn Thr Leu His Ile Gly Asn Asn		
335	340	345
Arg Val Ser Tyr Ile Ala Asp Cys Ala Phe Arg Gly Leu Ser Ser		
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Leu Lys Thr Leu Asp Leu Lys Asn Asn Glu Ile Ser Trp Thr Ile		
365	370	375
Glu Asp Met Asn Gly Ala Phe Ser Gly Leu Asp Lys Leu Arg Arg		
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395	400	405
Phe Thr Gly Leu Asp Ala Leu Glu His Leu Asp Leu Ser Asp Asn		
410	415	420
Ala Ile Met Ser Leu Gln Gly Asn Ala Phe Ser Gln Met Lys Lys		
425	430	435
Leu Gln Gln Leu His Leu Asn Thr Ser Ser Leu Leu Cys Asp Cys		
440	445	450
Gln Leu Lys Trp Leu Pro Gln Trp Val Ala Glu Asn Asn Phe Gln		
455	460	465
Ser Phe Val Asn Ala Ser Cys Ala His Pro Gln Leu Leu Lys Gly		
470	475	480

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 His Phe Gly Ser Ser Tyr Ser Val Lys Ala Lys Leu Thr Val Asn  
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 620 625 630  
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 635 640 645  
 Ala Ala Arg Glu Arg Arg Met His Val Met Pro Glu Asp Asp Val  
 650 655 660  
 Phe Phe Ile Val Asp Val Lys Ile Glu Asp Ile Gly Val Tyr Ser  
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 Cys Thr Ala Gln Asn Ser Ala Gly Ser Ile Ser Ala Asn Ala Thr  
 680 685 690  
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 695 700 705  
 Arg Thr Val Thr Lys Gly Glu Thr Ala Val Leu Gln Cys Ile Ala  
 710 715 720  
 Gly Gly Ser Pro Pro Pro Lys Leu Asn Trp Thr Lys Asp Asp Ser  
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 Pro Leu Val Val Thr Glu Arg His Phe Phe Ala Ala Gly Asn Gln  
 740 745 750

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 860 865 870  
 Tyr Val Ser Ser Glu Ser Gly Ser His His Gln Phe Val Thr Ser  
 875 880 885  
 Ser Gly Ala Gly Phe Phe Leu Pro Gln His Asp Ser Ser Gly Thr  
 890 895 900  
 Cys His Ile Asp Asn Ser Ser Glu Ala Asp Val Glu Ala Ala Thr  
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 980 985 990  
 Pro Ser His Val Arg Lys Leu Leu Asn Thr Ser Tyr Ser His Asn  
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Asp Ala Tyr Ser Ser Phe Gly Gln Pro Ser Asp Cys Gln Pro Arg  
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Ala Phe Tyr Leu Lys Ala His Ser Ser Pro Asp Leu Asp Ser Gly  
1070                    1075                    1080  
Ser Glu Glu Asp Gly Lys Glu Arg Thr Asp Phe Gln Glu Glu Asn  
1085                    1090                    1095  
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&lt;210&gt; 296

&lt;211&gt; 19

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&lt;213&gt; Artificial Sequence

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&lt;400&gt; 296

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&lt;210&gt; 297

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&lt;212&gt; DNA

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gcacagagag ggtggccgacc agctgttctc catatgcact aagaatagaa 1900  
caagagggaaa ctggcttaga cttagtata agggagcatt tcttggcagg 1950  
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aat 3003

<210> 315

<211> 509

<212> PRT

<213> Homo Sapien

<400> 315		
Met Asp Phe Leu Leu Ala Leu Val Leu Val Ser Ser Leu Tyr Leu		
1	5	15
Gln Ala Ala Ala Glu Phe Asp Gly Arg Trp Pro Arg Gln Ile Val		
20	25	30
Ser Ser Ile Gly Leu Cys Arg Tyr Gly Gly Arg Ile Asp Cys Cys		
35	40	45
Trp Gly Trp Ala Arg Gln Ser Trp Gly Gln Cys Gln Pro Val Cys		
50	55	60
Gln Pro Arg Cys Lys His Gly Glu Cys Ile Gly Pro Asn Lys Cys		
65	70	75
Lys Cys His Pro Gly Tyr Ala Gly Lys Thr Cys Asn Gln Asp Leu		
80	85	90
Asn Glu Cys Gly Leu Lys Pro Arg Pro Cys Lys His Arg Cys Met		
95	100	105
Asn Thr Tyr Gly Ser Tyr Lys Cys Tyr Cys Leu Asn Gly Tyr Met		
110	115	120
Leu Met Pro Asp Gly Ser Cys Ser Ser Ala Leu Thr Cys Ser Met		
125	130	135
Ala Asn Cys Gln Tyr Gly Cys Asp Val Val Lys Gly Gln Ile Arg		
140	145	150
Cys Gln Cys Pro Ser Pro Gly Leu His Leu Ala Pro Asp Gly Arg		
155	160	165

Thr Cys Val Asp Val Asp Glu Cys Ala Thr Gly Arg Ala Ser Cys  
 170 175 180  
 Pro Arg Phe Arg Gln Cys Val Asn Thr Phe Gly Ser Tyr Ile Cys  
 185 190 195  
 Lys Cys His Lys Gly Phe Asp Leu Met Tyr Ile Gly Gly Lys Tyr  
 200 205 210  
 Gln Cys His Asp Ile Asp Glu Cys Ser Leu Gly Gln Tyr Gln Cys  
 215 220 225  
 Ser Ser Phe Ala Arg Cys Tyr Asn Val Arg Gly Ser Tyr Lys Cys  
 230 235 240  
 Lys Cys Lys Glu Gly Tyr Gln Gly Asp Gly Leu Thr Cys Val Tyr  
 245 250 255  
 Ile Pro Lys Val Met Ile Glu Pro Ser Gly Pro Ile His Val Pro  
 260 265 270  
 Lys Gly Asn Gly Thr Ile Leu Lys Gly Asp Thr Gly Asn Asn Asn  
 275 280 285  
 Trp Ile Pro Asp Val Gly Ser Thr Trp Trp Pro Pro Lys Thr Pro  
 290 295 300  
 Tyr Ile Pro Pro Ile Ile Thr Asn Arg Pro Thr Ser Lys Pro Thr  
 305 310 315  
 Thr Arg Pro Thr Pro Lys Pro Thr Pro Ile Pro Thr Pro Pro Pro  
 320 325 330  
 Pro Pro Pro Leu Pro Thr Glu Leu Arg Thr Pro Leu Pro Pro Thr  
 335 340 345  
 Thr Pro Glu Arg Pro Thr Thr Gly Leu Thr Thr Ile Ala Pro Ala  
 350 355 360  
 Ala Ser Thr Pro Pro Gly Gly Ile Thr Val Asp Asn Arg Val Gln  
 365 370 375  
 Thr Asp Pro Gln Lys Pro Arg Gly Asp Val Phe Ser Val Leu Val  
 380 385 390  
 His Ser Cys Asn Phe Asp His Gly Leu Cys Gly Trp Ile Arg Glu  
 395 400 405  
 Lys Asp Asn Asp Leu His Trp Glu Pro Ile Arg Asp Pro Ala Gly  
 410 415 420  
 Gly Gln Tyr Leu Thr Val Ser Ala Ala Lys Ala Pro Gly Gly Lys

425	430	435
Ala Ala Arg Leu Val Leu Pro Leu Gly Arg Leu Met His Ser Gly		
440	445	450
Asp Leu Cys Leu Ser Phe Arg His Lys Val Thr Gly Leu His Ser		
455	460	465
Gly Thr Leu Gln Val Phe Val Arg Lys His Gly Ala His Gly Ala		
470	475	480
Ala Leu Trp Gly Arg Asn Gly Gly His Gly Trp Arg Gln Thr Gln		
485	490	495
Ile Thr Leu Arg Gly Ala Asp Ile Lys Ser Glu Ser Gln Arg		
500	505	

<210> 316

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 316

gatggttcct gctcaagtgc cctg 24

<210> 317

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 317

ttgcacttgt aggacccacg tacg 24

<210> 318

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 318

ctgatggag gacctgtgta gatgttgatg aatgtgctac aggaagagcc 50

<210> 319

<211> 2110

<212> DNA

<213> Homo Sapien

<400> 319  
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caacaggtgc ttgctcgaaa ctgaaggtga cagtgccatc acacactgtc 150  
catggcgtca gaggtcaggc cctctaccta cccgtccact atggcttcca 200  
cactccagca tcagacatcc agatcatatg gctattttag agaccccaca 250  
caatgccccaa atacttactg ggctctgtga ataagtctgt ggttcctgac 300  
ttgaaatacc aacacaagtt caccatgatg ccacccaatg catctctgct 350  
tatcaaccca ctgcagttcc ctgatgaagg caattacatc gtgaaggtca 400  
acattcaggg aaatgaaact ctatctgcca gtcagaagat acaagtcacg 450  
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atccccccaa cacctactcc tggatttagga ggactgacaa tactacatat 900  
atcattaagc atgggcctcg cttagaaagtt gcatctgaga aagtagccca 950  
gaagacaatg gactatgtgt gctgtgctta caacaacata accggcaggc 1000  
aagatgaaac tcatttcaca gttatcatca ctcccgtagg actggagaag 1050  
cttgcacaga aaggaaaatc attgtcaccc tttagcaagta taactggaat 1100  
atcactattt ttgatttatat ccatgtgtct tctcttccta tggaaaaaat 1150  
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gaatacagga aagctcaaac attttcaggc catgaagatg ctctggatga 1250

cttcggata tatgaatttg ttgctttcc agatgttct ggtgtttcca 1300  
 ggattccaag caggtctgtt ccagcctctg attgtgtatc ggggcaagat 1350  
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 agaccatcca gagtgaactt tcatgggcta aacagtacat tcgagtgaaa 1450  
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 aatcagtgaa gaaaccagga ccaacacctc ttactcatta ttcctttaca 1550  
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 tttatttagtg ttaagaatgc taaatttatg tttcaatttt atttccaaat 1900  
 ttctatcttg ttatttgtac aacaaagtaa taaggatggt tgcacaaaa 1950  
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 agacttgcga acacttaagg aaatgactat taaagtctta tttttatttt 2050  
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<210> 320  
 <211> 450  
 <212> PRT  
 <213> Homo Sapien

<400> 320				
Met Trp Leu Lys Val Phe Thr Thr Phe Leu Ser Phe Ala Thr Gly				
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Ala Cys Ser Gly Leu Lys Val Thr Val Pro Ser His Thr Val His				
20	25			30
Gly Val Arg Gly Gln Ala Leu Tyr Leu Pro Val His Tyr Gly Phe				
35	40			45
His Thr Pro Ala Ser Asp Ile Gln Ile Ile Trp Leu Phe Glu Arg				
50	55			60

Pro His Thr Met Pro Lys Tyr Leu Leu Gly Ser Val Asn Lys Ser  
                   65                     70                     75

Val Val Pro Asp Leu Glu Tyr Gln His Lys Phe Thr Met Met Pro  
                   80                     85                     90

Pro Asn Ala Ser Leu Leu Ile Asn Pro Leu Gln Phe Pro Asp Glu  
                   95                     100                    105

Gly Asn Tyr Ile Val Lys Val Asn Ile Gln Gly Asn Gly Thr Leu  
                   110                    115                    120

Ser Ala Ser Gln Lys Ile Gln Val Thr Val Asp Asp Pro Val Thr  
                   125                    130                    135

Lys Pro Val Val Gln Ile His Pro Pro Ser Gly Ala Val Glu Tyr  
                   140                    145                    150

Val Gly Asn Met Thr Leu Thr Cys His Val Glu Gly Gly Thr Arg  
                   155                    160                    165

Leu Ala Tyr Gln Trp Leu Lys Asn Gly Arg Pro Val His Thr Ser  
                   170                    175                    180

Ser Thr Tyr Ser Phe Ser Pro Gln Asn Asn Thr Leu His Ile Ala  
                   185                    190                    195

Pro Val Thr Lys Glu Asp Ile Gly Asn Tyr Ser Cys Leu Val Arg  
                   200                    205                    210

Asn Pro Val Ser Glu Met Glu Ser Asp Ile Ile Met Pro Ile Ile  
                   215                    220                    225

Tyr Tyr Gly Pro Tyr Gly Leu Gln Val Asn Ser Asp Lys Gly Leu  
                   230                    235                    240

Lys Val Gly Glu Val Phe Thr Val Asp Leu Gly Glu Ala Ile Leu  
                   245                    250                    255

Phe Asp Cys Ser Ala Asp Ser His Pro Pro Asn Thr Tyr Ser Trp  
                   260                    265                    270

Ile Arg Arg Thr Asp Asn Thr Thr Tyr Ile Ile Lys His Gly Pro  
                   275                    280                    285

Arg Leu Glu Val Ala Ser Glu Lys Val Ala Gln Lys Thr Met Asp  
                   290                    295                    300

Tyr Val Cys Cys Ala Tyr Asn Asn Ile Thr Gly Arg Gln Asp Glu  
                   305                    310                    315

Thr His Phe Thr Val Ile Ile Thr Ser Val Gly Leu Glu Lys Leu

320	325	330
Ala Gln Lys Gly Lys Ser Leu Ser Pro Leu Ala Ser Ile Thr Gly		
335	340	345
Ile Ser Leu Phe Leu Ile Ile Ser Met Cys Leu Leu Phe Leu Trp		
350	355	360
Lys Lys Tyr Gln Pro Tyr Lys Val Ile Lys Gln Lys Leu Glu Gly		
365	370	375
Arg Pro Glu Thr Glu Tyr Arg Lys Ala Gln Thr Phe Ser Gly His		
380	385	390
Glu Asp Ala Leu Asp Asp Phe Gly Ile Tyr Glu Phe Val Ala Phe		
395	400	405
Pro Asp Val Ser Gly Val Ser Arg Ile Pro Ser Arg Ser Val Pro		
410	415	420
Ala Ser Asp Cys Val Ser Gly Gln Asp Leu His Ser Thr Val Tyr		
425	430	435
Glu Val Ile Gln His Ile Pro Ala Gln Gln Asp His Pro Glu		
440	445	450

<210> 321

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 321

gatcctgtca caaagccagt ggtgc 25

<210> 322

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 322

cactgacagg gttcctcacc cagg 24

<210> 323

<211> 45

<212> DNA

<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe  
  
<400> 323  
ctccctctgg gctgtggagt atgtgggaa catgaccctg acatg 45  
  
<210> 324  
<211> 2397  
<212> DNA  
<213> Homo Sapien  
  
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acgttcgcgt catcacggac gagaactgga gagaactgct ggaaggagac 150  
tggatgatag aattttatgc cccgtggtgc cctgcttgc aaaatcttca 200  
accggaatgg gaaaatggg ctgaatgggg agaagatctt gaggttaata 250  
ttgcgaaagt agatgtcaca gaggcagccag gactgagtgg acggtttatac 300  
ataactgctc ttcctactat ttatcattgt aaagatggtg aatttagggc 350  
ctatcagggt ccaaggacta agaaggactt cataaacttt ataagtgata 400  
aagagtggaa gagtattgag cccgtttcat catggttgg tccaggttct 450  
gttctgatga gtagtatgtc agcaactttt cagctatcta tgtggatcag 500  
gacgtgccat aactactta ttgaagacct tggattgcca gtgtgggat 550  
catatactgt tttgcttta gcaactctgt tttccggact gttatttagga 600  
ctctgtatga tatttgtggc agattgcctt tgtccttcaa aaaggcgcag 650  
accacagcca tacccatacc cttcaaaaaa attattatca gaatctgcac 700  
aacctttgaa aaaagtggag gaggaacaag aggccggatga agaagatgtt 750  
tcagaagaag aagctgaaag taaagaagga acaaacaag actttccaca 800  
gaatgccata agacaacgct ctctgggtcc atcattggcc acagataaat 850  
cctagttaaa ttttatagtt atcttaatat tatgattttg ataaaaacag 900  
aagattgatc attttgtttg gtttgaagtg aactgtgact ttttgaata 950  
ttgcagggtt cagtctagat tgtcattaaa ttgaagagtc tacattcaga 1000

acataaaaagc actaggata caagttgaa atatgattt agcacagtat 1050  
gatggtttaa atagttctct aattttgaa aaatcgcc aagcaataag 1100  
atttatgtat atttggtaa taataaccta tttcaagtct gagtttgaa 1150  
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agaaaatgtgt atttcagtga caatttcgtg gtcttttag aggtatattc 1350  
caaaatttcc ttgtatTTT aggttatgca actaataaaa actaccttac 1400  
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ctgaccatta cgttagtagac aatttctgta atgtccccctt ctttcttaggc 2200  
tctgttgctg tgtgaatcca ttagattac agtacgtaa tatacaagtt 2250  
ttctttaaag ccctctcctt tagaatttaa aatattgtac cattaaagag 2300  
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aaaccttctt aaccacttca ttaaagctga aaaaaaaaaa aaaaaaaaa 2397

<210> 325

<211> 280

<212> PRT

<213> Homo Sapien

<400> 325

Met	Ala	Pro	Ser	Gly	Ser	Leu	Ala	Val	Pro	Leu	Ala	Val	Leu	Val
1														
						5			10					15

Leu	Leu	Leu	Trp	Gly	Ala	Pro	Trp	Thr	His	Gly	Arg	Arg	Ser	Asn
			20						25					30

Val	Arg	Val	Ile	Thr	Asp	Glu	Asn	Trp	Arg	Glu	Leu	Leu	Glu	Gly
			35						40					45

Asp	Trp	Met	Ile	Glu	Phe	Tyr	Ala	Pro	Trp	Cys	Pro	Ala	Cys	Gln
			50						55					60

Asn	Leu	Gln	Pro	Glu	Trp	Glu	Ser	Phe	Ala	Glu	Trp	Gly	Glu	Asp
			65						70					75

Leu	Glu	Val	Asn	Ile	Ala	Lys	Val	Asp	Val	Thr	Glu	Gln	Pro	Gly
			80						85					90

Leu	Ser	Gly	Arg	Phe	Ile	Ile	Thr	Ala	Leu	Pro	Thr	Ile	Tyr	His
			95						100					105

Cys	Lys	Asp	Gly	Glu	Phe	Arg	Arg	Tyr	Gln	Gly	Pro	Arg	Thr	Lys
			110						115					120

Lys	Asp	Phe	Ile	Asn	Phe	Ile	Ser	Asp	Lys	Glu	Trp	Lys	Ser	Ile
			125						130					135

Glu	Pro	Val	Ser	Ser	Trp	Phe	Gly	Pro	Gly	Ser	Val	Leu	Met	Ser
			140						145					150

Ser	Met	Ser	Ala	Leu	Phe	Gln	Leu	Ser	Met	Trp	Ile	Arg	Thr	Cys
			155						160					165

His	Asn	Tyr	Phe	Ile	Glu	Asp	Leu	Gly	Leu	Pro	Val	Trp	Gly	Ser
			170						175					180

Tyr	Thr	Val	Phe	Ala	Leu	Ala	Thr	Leu	Phe	Ser	Gly	Leu	Leu	
			185						190					195

Gly	Leu	Cys	Met	Ile	Phe	Val	Ala	Asp	Cys	Leu	Cys	Pro	Ser	Lys
			200						205					210

Arg Arg Arg Pro Gln Pro Tyr Pro Tyr Pro Ser Lys Lys Leu Leu

215	220	225
Ser Glu Ser Ala Gln Pro Leu Lys Lys Val Glu Glu Glu Gln Glu		
230	235	240
Ala Asp Glu Glu Asp Val Ser Glu Glu Ala Glu Ser Lys Glu		
245	250	255
Gly Thr Asn Lys Asp Phe Pro Gln Asn Ala Ile Arg Gln Arg Ser		
260	265	270
Leu Gly Pro Ser Leu Ala Thr Asp Lys Ser		
275	280	

<210> 326  
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<212> DNA  
  
<213> Artificial Sequence  
  
<220>  
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<223> Synthetic Oligonucleotide Probe  
  
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tatgtggatc aggacgtgcc 20  
  
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<212> DNA  
<213> Homo Sapien  
  
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ggaccaggc acaatttcca gaggggaact tccaggaacc aagtaccagg 650  
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gaaggggact attatcatac ggtgttggg atggagcagg tgctaaagca 750

gcttgatgcc ggggaggagg ccaccacaac caagtcacag gtgctggact 800  
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gtctgatgag gaaatcgaga ggatcaagga gatcgaaaa cctaaacttg 1250  
cacgagccac cggtcgat cccaagacag gagtcctcac tgccgcagc 1300  
taccgggttt ccaaaagctc ctggcttagag gaagatgtatg accctgttgt 1350  
ggcccgagta aatcgctgga tgcagcatat cacagggta acagtaaaga 1400  
ctgcagaatt gttacaggtt gcaaattatg gagtgggagg acagtatgaa 1450  
ccgcacttcg acttctctag gcgacccttt gacagcggcc tcaaaacaga 1500  
ggggaaatagg tttagcgacgt ttcttaacta catgagtgtat gttagagctg 1550  
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ggtacagctg tggctggta caacctcttggg cggagcgggg aaggtgacta 1650  
ccgaacaaga catgctgcct gccctgtgtc tgtggctgc aagtgggtct 1700  
ccaataagtg gttccatgaa cgaggacagg agtttttgag accttggta 1750  
tcaacagaag ttgactgaca tcctttctg tccttccct tcctggct 1800  
tcagccccatg tcaacgtgac agacacctt gtatgttccct ttgtatgtc 1850  
ctatcaggct gatttttggaa gaaatgaatg tttgtctggaa gcagagggag 1900  
accataactag ggcgactcct gtgtgactga agtcccagcc cttccattca 1950  
gcctgtgcca tccctggccc caaggctagg atcaaagtgg ctgcagcaga 2000  
gttagctgtc tagcgccctag caaggtgcct ttgtacctca ggtgttttag 2050  
gtgtgagatg tttcagtgaa ccaaagttct gataccttgtt ttacatgttt 2100

gttttatgg catttctatc tattgtggct ttaccaaaaa ataaaatgtc 2150

cctaccagaa aaaaaaaaa 2168

<210> 332

<211> 533

<212> PRT

<213> Homo Sapien

<400> 332

Met	Lys	Leu	Trp	Val	Ser	Ala	Leu	Leu	Met	Ala	Trp	Phe	Gly	Val
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Leu	Ser	Cys	Val	Gln	Ala	Glu	Phe	Phe	Thr	Ser	Ile	Gly	His	Met
									20					30

Thr	Asp	Leu	Ile	Tyr	Ala	Glu	Glu	Leu	Val	Gln	Ser	Leu	Lys
									35				45

Glu	Tyr	Ile	Leu	Val	Glu	Glu	Ala	Lys	Leu	Ser	Lys	Ile	Lys	Ser
									50			55		60

Trp	Ala	Asn	Lys	Met	Glu	Ala	Leu	Thr	Ser	Lys	Ser	Ala	Ala	Asp
									65			70		75

Ala	Glu	Gly	Tyr	Leu	Ala	His	Pro	Val	Asn	Ala	Tyr	Lys	Leu	Val
									80			85		90

Lys	Arg	Leu	Asn	Thr	Asp	Trp	Pro	Ala	Leu	Glu	Asp	Leu	Val	Leu
									95			100		105

Gln	Asp	Ser	Ala	Ala	Gly	Phe	Ile	Ala	Asn	Leu	Ser	Val	Gln	Arg
									110			115		120

Gln	Phe	Phe	Pro	Thr	Asp	Glu	Asp	Glu	Ile	Gly	Ala	Ala	Lys	Ala
									125			130		135

Leu	Met	Arg	Leu	Gln	Asp	Thr	Tyr	Arg	Leu	Asp	Pro	Gly	Thr	Ile
									140			145		150

Ser	Arg	Gly	Glu	Leu	Pro	Gly	Thr	Lys	Tyr	Gln	Ala	Met	Leu	Ser
									155			160		165

Val	Asp	Asp	Cys	Phe	Gly	Met	Gly	Arg	Ser	Ala	Tyr	Asn	Glu	Gly
									170			175		180

Asp	Tyr	Tyr	His	Thr	Val	Leu	Trp	Met	Glu	Gln	Val	Leu	Lys	Gln
									185			190		195

Leu	Asp	Ala	Gly	Glu	Glu	Ala	Thr	Thr	Lys	Ser	Gln	Val	Leu	
									200			205		210

Asp Tyr Leu Ser Tyr Ala Val Phe Gln Leu Gly Asp Leu His Arg  
 215 220 225  
 Ala Leu Glu Leu Thr Arg Arg Leu Leu Ser Leu Asp Pro Ser His  
 230 235 240  
 Glu Arg Ala Gly Gly Asn Leu Arg Tyr Phe Glu Gln Leu Leu Glu  
 245 250 255  
 Glu Glu Arg Glu Lys Thr Leu Thr Asn Gln Thr Glu Ala Glu Leu  
 260 265 270  
 Ala Thr Pro Glu Gly Ile Tyr Glu Arg Pro Val Asp Tyr Leu Pro  
 275 280 285  
 Glu Arg Asp Val Tyr Glu Ser Leu Cys Arg Gly Glu Gly Val Lys  
 290 295 300  
 Leu Thr Pro Arg Arg Gln Lys Arg Leu Phe Cys Arg Tyr His His  
 305 310 315  
 Gly Asn Arg Ala Pro Gln Leu Leu Ile Ala Pro Phe Lys Glu Glu  
 320 325 330  
 Asp Glu Trp Asp Ser Pro His Ile Val Arg Tyr Tyr Asp Val Met  
 335 340 345  
 Ser Asp Glu Glu Ile Glu Arg Ile Lys Glu Ile Ala Lys Pro Lys  
 350 355 360  
 Leu Ala Arg Ala Thr Val Arg Asp Pro Lys Thr Gly Val Leu Thr  
 365 370 375  
 Val Ala Ser Tyr Arg Val Ser Lys Ser Ser Trp Leu Glu Glu Asp  
 380 385 390  
 Asp Asp Pro Val Val Ala Arg Val Asn Arg Arg Met Gln His Ile  
 395 400 405  
 Thr Gly Leu Thr Val Lys Thr Ala Glu Leu Leu Gln Val Ala Asn  
 410 415 420  
 Tyr Gly Val Gly Gly Gln Tyr Glu Pro His Phe Asp Phe Ser Arg  
 425 430 435  
 Arg Pro Phe Asp Ser Gly Leu Lys Thr Glu Gly Asn Arg Leu Ala  
 440 445 450  
 Thr Phe Leu Asn Tyr Met Ser Asp Val Glu Ala Gly Gly Ala Thr  
 455 460 465  
 Val Phe Pro Asp Leu Gly Ala Ala Ile Trp Pro Lys Lys Gly Thr  
 470 475 480

Ala Val Phe Trp Tyr Asn Leu Leu Arg Ser Gly Glu Gly Asp Tyr  
485 490 495  
Arg Thr Arg His Ala Ala Cys Pro Val Leu Val Gly Cys Lys Trp  
500 505 510  
Val Ser Asn Lys Trp Phe His Glu Arg Gly Gln Glu Phe Leu Arg  
515 520 525  
Pro Cys Gly Ser Thr Glu Val Asp  
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<210> 333

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 333

ccaggcacaa tttccaga 18

<210> 334

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 334

ggacccttct gtgtgccag 19

<210> 335

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 335

ggtctcaaga actcctgtc 19

<210> 336

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 336  
acactcagca ttgcctggta cttg 24

<210> 337  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 337  
gggcacatga ctgacacctgat ttatgcagag aaagagctgg tgcag 45

<210> 338  
<211> 2789

<212> DNA  
<213> Homo Sapien

<400> 338  
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tcccaagtgtg agtggaaattt attgtttcat ttattaccgt tttggctggg 100  
ggtagttcc gacaccccca cagttggaaaga gcaggcagaa ggagttgtga 150  
agacaggaca atcttottgg ggtatgcgtt cctggaaagcc agcgggcctt 200  
gctctgtctt tggcctcatt gaccccagggt tctctggta aaactgaaag 250  
cctactactg gcctggtgcc catcaatcca ttgatccttgg 300  
cctggggcac ccacccggca gggcctacca ccatgcgact gagctccctg 350  
ttggctctgc tgccggccaggc gcttccctc atcttagggc tgcgtctggg 400  
gtgcaggctg agcctccctgc gggtttccctg gatccagggg gagggagaag 450  
atccctgtgt cgaggctgtt ggggagcgag gagggccaca gaatccagat 500  
tcgagagctc ggcttagacca aagtgtatgaa gacttcaaacc cccggattgt 550  
ccccctactac agggacccca acaaggcccta caagaagggtg ctcaggactc 600  
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cccgccctcc agcaggatg caggtggtgtt ctcatgggta tgagcggcccc 800

gcctggctca tgcagagac cctgcgccac cttcacacac actttggggc 850  
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ccgcctggc agcccttgct ggccacctca gcatcaacca agacctgtac 950  
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acagcaccag gggcagcagt atcgctcatt tgaactggcc aaaaataggg 1200  
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tctggagttg gagcgggctt acagtgaaat agaacaactg caggctcaga 1350  
tccggAACCT gaccgtgctg acccccgaag gggaggcagg gctgagctgg 1400  
cccgtgggc tccctgctcc tttcacacca cactctcgct ttgaggtgct 1450  
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gcccagctgg gggccctaac ctcattacct ttccttgc tgcctcagcc 2700  
ccaggaaggg caaggcaaga tggtgacag atagagaatt gttgtgtat 2750  
tttttaaaaata tqaaaatqtt attaaacatg tcttcgtcc 2789

<210> 339  
<211> 772  
<212> PRT  
<213> Homo Sapien

<400> 339  
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Leu Ile Leu Gly Leu Ser Leu Gly Cys Ser Leu Ser Leu Leu Arg  
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Val Ser Trp Ile Gln Gly Glu Gly Glu Asp Pro Cys Val Glu Ala  
35 40 45

Val Gly Glu Arg Gly Gly Pro Gln Asn Pro Asp Ser Arg Ala Arg  
50 55 60

Leu Asp Gln Ser Asp Glu Asp Phe Lys Pro Arg Ile Val Pro Tyr  
65 70 75

Tyr Arg Asp Pro Asn Lys Pro Tyr Lys Lys Val Leu Arg Thr Arg  
80 85 90

Tyr Ile Gln Thr Glu Leu Gly Ser Arg Glu Arg Leu Leu Val Ala

95	100	105
Val Leu Thr Ser Arg Ala Thr Leu Ser	Thr Leu Ala Val Ala Val	
110	115	120
Asn Arg Thr Val Ala His His Phe Pro	Arg Leu Leu Tyr Phe Thr	
125	130	135
Gly Gln Arg Gly Ala Arg Ala Pro Ala	Gly Met Gln Val Val Ser	
140	145	150
His Gly Asp Glu Arg Pro Ala Trp	Leu Met Ser Glu Thr Leu Arg	
155	160	165
His Leu His Thr His Phe Gly Ala Asp	Tyr Asp Trp Phe Phe Ile	
170	175	180
Met Gln Asp Asp Thr Tyr Val Gln Ala	Pro Arg Leu Ala Ala Leu	
185	190	195
Ala Gly His Leu Ser Ile Asn Gln Asp	Leu Tyr Leu Gly Arg Ala	
200	205	210
Glu Glu Phe Ile Gly Ala Gly Glu Gln Ala	Arg Tyr Cys His Gly	
215	220	225
Gly Phe Gly Tyr Leu Leu Ser Arg Ser	Leu Leu Leu Arg Leu Arg	
230	235	240
Pro His Leu Asp Gly Cys Arg Gly Asp	Ile Leu Ser Ala Arg Pro	
245	250	255
Asp Glu Trp Leu Gly Arg Cys Leu Ile Asp	Ser Leu Gly Val Gly	
260	265	270
Cys Val Ser Gln His Gln Gly Gln Gln	Tyr Arg Ser Phe Glu Leu	
275	280	285
Ala Lys Asn Arg Asp Pro Glu Lys Glu Gly	Ser Ser Ala Phe Leu	
290	295	300
Ser Ala Phe Ala Val His Pro Val Ser	Glu Gly Thr Leu Met Tyr	
305	310	315
Arg Leu His Lys Arg Phe Ser Ala Leu	Glu Leu Glu Arg Ala Tyr	
320	325	330
Ser Glu Ile Glu Gln Leu Gln Ala Gln	Ile Arg Asn Leu Thr Val	
335	340	345
Leu Thr Pro Glu Gly Glu Ala Gly Leu	Ser Trp Pro Val Gly Leu	
350	355	360

Pro Ala Pro Phe Thr Pro His Ser Arg Phe Glu Val Leu Gly Trp  
 365 370 375  
 Asp Tyr Phe Thr Glu Gln His Thr Phe Ser Cys Ala Asp Gly Ala  
 380 385 390  
 Pro Lys Cys Pro Leu Gln Gly Ala Ser Arg Ala Asp Val Gly Asp  
 395 400 405  
 Ala Leu Glu Thr Ala Leu Glu Gln Leu Asn Arg Arg Tyr Gln Pro  
 410 415 420  
 Arg Leu Arg Phe Gln Lys Gln Arg Leu Leu Asn Gly Tyr Arg Arg  
 425 430 435  
 Phe Asp Pro Ala Arg Gly Met Glu Tyr Thr Leu Asp Leu Leu Leu  
 440 445 450  
 Glu Cys Val Thr Gln Arg Gly His Arg Arg Ala Leu Ala Arg Arg  
 455 460 465  
 Val Ser Leu Leu Arg Pro Leu Ser Arg Val Glu Ile Leu Pro Met  
 470 475 480  
 Pro Tyr Val Thr Glu Ala Thr Arg Val Gln Leu Val Leu Pro Leu  
 485 490 495  
 Leu Val Ala Glu Ala Ala Ala Pro Ala Phe Leu Glu Ala Phe  
 500 505 510  
 Ala Ala Asn Val Leu Glu Pro Arg Glu His Ala Leu Leu Thr Leu  
 515 520 525  
 Leu Leu Val Tyr Gly Pro Arg Glu Gly Gly Arg Gly Ala Pro Asp  
 530 535 540  
 Pro Phe Leu Gly Val Lys Ala Ala Ala Ala Glu Leu Glu Arg Arg  
 545 550 555  
 Tyr Pro Gly Thr Arg Leu Ala Trp Leu Ala Val Arg Ala Glu Ala  
 560 565 570  
 Pro Ser Gln Val Arg Leu Met Asp Val Val Ser Lys Lys His Pro  
 575 580 585  
 Val Asp Thr Leu Phe Phe Leu Thr Thr Val Trp Thr Arg Pro Gly  
 590 595 600  
 Pro Glu Val Leu Asn Arg Cys Arg Met Asn Ala Ile Ser Gly Trp  
 605 610 615  
 Gln Ala Phe Phe Pro Val His Phe Gln Glu Phe Asn Pro Ala Leu  
 620 625 630

Ser Pro Gln Arg Ser Pro Pro Gly Pro Pro Gly Ala Gly Pro Asp  
 635 640 645  
 Pro Pro Ser Pro Pro Gly Ala Asp Pro Ser Arg Gly Ala Pro Ile  
 650 655 660  
 Gly Gly Arg Phe Asp Arg Gln Ala Ser Ala Glu Gly Cys Phe Tyr  
 665 670 675  
 Asn Ala Asp Tyr Leu Ala Ala Arg Ala Arg Leu Ala Gly Glu Leu  
 680 685 690  
 Ala Gly Gln Glu Glu Glu Ala Leu Glu Gly Leu Glu Val Met  
 695 700 705  
 Asp Val Phe Leu Arg Phe Ser Gly Leu His Leu Phe Arg Ala Val  
 710 715 720  
 Glu Pro Gly Leu Val Gln Lys Phe Ser Leu Arg Asp Cys Ser Pro  
 725 730 735  
 Arg Leu Ser Glu Glu Leu Tyr His Arg Cys Arg Leu Ser Asn Leu  
 740 745 750  
 Glu Gly Leu Gly Gly Arg Ala Gln Leu Ala Met Ala Leu Phe Glu  
 755 760 765  
 Gln Glu Gln Ala Asn Ser Thr  
 770

<210> 340  
 <211> 1572  
 <212> DNA  
 <213> Homo Sapien

<400> 340  
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 tgtccccaaag ccgtttctaga cgcggaaaa atgcgttctg aaagcagctc 100  
 ctttttgaag ggtgtatgc ttggaagcat tttctgtgct ttgatcacta 150  
 tgctaggaca cattaggatt ggtcatggaa atagaatgca ccaccatgag 200  
 catcatcacc tacaagctcc taacaaagaa gatatcttga aaatttcaga 250  
 ggatgagcgc atggagctca gtaagagctt tcgagttatac tgtattatcc 300  
 ttgtaaaacc caaagatgtg agtcttggg ctgcagtaaa ggagacttgg 350  
 accaaacact gtgacaaaagc agagttcttc agttctgaaa atgttaaagt 400

gttgagtca attaatatgg acacaaatga catgtggta atgatgagaa 450  
aagcttacaa atacgcctt gataagtata gagaccaata caactggttc 500  
ttcctgcac gccccactac gttgctatc attgaaaacc taaagtattt 550  
tttgttaaaa aaggatccat cacagcctt ctatctaggc cacactataa 600  
aatctggaga ccttgaatat gtgggtatgg aaggaggaat tgtcttaagt 650  
gtagaatcaa tgaaaagact taacagcctt ctcaatatcc cagaaaagtg 700  
tcctgaacag ggagggatga tttggaagat atctgaagat aaacagctag 750  
cagttgcct gaaatatgct ggagtattt cagaaaatgc agaagatgct 800  
gatggaaaag atgtatttaa taccaaattct gttggcttt ctattaaaga 850  
ggcaatgact tatkaccccc accaggtgt agaaggctgt tgtagata 900  
tggctgttac tttaatgga ctgactccaa atcagatgca tgtgatgatg 950  
tatgggtat accgccttag ggcatttggg catatttca atgatgcatt 1000  
ggtttctta cctccaaatg gttctgacaa tgactgagaa gtggtagaaa 1050  
agcgtgaata tgatcttgt ataggacgtg tgtagtcatt attttagta 1100  
gtaactacat atccaataca gctgtatgtt tcttttctt ttctaattt 1150  
gtggcactgg tataaccaca cattaaagtc agtagtacat tttaaatga 1200  
gggtggttt ttttttaaaa acacatgaac attgtaaatg tgtagaaag 1250  
aagtgtttta agaataataa ttttgc当地 aaactattaa taaatattat 1300  
atgtgataaa ttctaaatta tgaacattag aaatctgtgg ggcacatatt 1350  
tttgctgatt ggttaaaaaa tttaacagg tcttagcgt tctaagat 1400  
gcaaatgata tctctagttg tgaatttgcgt attaaagtaa aacttttagc 1450  
tgtgtgttcc cttaacttct aatactgatt tatgttctaa gcctcccaa 1500  
gttccaatgg atttgccttc tcaaaatgta caactaagca actaaagaaa 1550  
attaaagtga aagttgaaaa at 1572

<210> 341  
<211> 318  
<212> PRT  
<213> Homo Sapien

&lt;400&gt; 341

Met	Leu	Ser	Glu	Ser	Ser	Ser	Phe	Leu	Lys	Gly	Val	Met	Leu	Gly
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Ser	Ile	Phe	Cys	Ala	Leu	Ile	Thr	Met	Leu	Gly	His	Ile	Arg	Ile
		20						25				30		
Gly	His	Gly	Asn	Arg	Met	His	His	His	Glu	His	His	His	Leu	Gln
		35						40				45		
Ala	Pro	Asn	Lys	Glu	Asp	Ile	Leu	Lys	Ile	Ser	Glu	Asp	Glu	Arg
		50						55				60		
Met	Glu	Leu	Ser	Lys	Ser	Phe	Arg	Val	Tyr	Cys	Ile	Ile	Leu	Val
		65						70				75		
Lys	Pro	Lys	Asp	Val	Ser	Leu	Trp	Ala	Ala	Val	Lys	Glu	Thr	Trp
		80						85				90		
Thr	Lys	His	Cys	Asp	Lys	Ala	Glu	Phe	Phe	Ser	Ser	Glu	Asn	Val
		95						100				105		
Lys	Val	Phe	Glu	Ser	Ile	Asn	Met	Asp	Thr	Asn	Asp	Met	Trp	Leu
		110						115				120		
Met	Met	Arg	Lys	Ala	Tyr	Lys	Tyr	Ala	Phe	Asp	Lys	Tyr	Arg	Asp
		125						130				135		
Gln	Tyr	Asn	Trp	Phe	Phe	Leu	Ala	Arg	Pro	Thr	Thr	Phe	Ala	Ile
		140						145				150		
Ile	Glu	Asn	Leu	Lys	Tyr	Phe	Leu	Leu	Lys	Lys	Asp	Pro	Ser	Gln
		155						160				165		
Pro	Phe	Tyr	Leu	Gly	His	Thr	Ile	Lys	Ser	Gly	Asp	Leu	Glu	Tyr
		170						175				180		
Val	Gly	Met	Glu	Gly	Gly	Ile	Val	Leu	Ser	Val	Glu	Ser	Met	Lys
		185						190				195		
Arg	Leu	Asn	Ser	Leu	Leu	Asn	Ile	Pro	Glu	Lys	Cys	Pro	Glu	Gln
		200						205				210		
Gly	Gly	Met	Ile	Trp	Lys	Ile	Ser	Glu	Asp	Lys	Gln	Leu	Ala	Val
		215						220				225		
Cys	Leu	Lys	Tyr	Ala	Gly	Val	Phe	Ala	Glu	Asn	Ala	Glu	Asp	Ala
		230						235				240		
Asp	Gly	Lys	Asp	Val	Phe	Asn	Thr	Lys	Ser	Val	Gly	Leu	Ser	Ile
		245						250				255		
Lys	Glu	Ala	Met	Thr	Tyr	His	Pro	Asn	Gln	Val	Val	Glu	Gly	Cys

260

265

270

Cys Ser Asp Met Ala Val Thr Phe Asn Gly Leu Thr Pro Asn Gln  
275 280 285

Met His Val Met Met Tyr Gly Val Tyr Arg Leu Arg Ala Phe Gly  
290 295 300

His Ile Phe Asn Asp Ala Leu Val Phe Leu Pro Pro Asn Gly Ser  
305 310 315

Asp Asn Asp

<210> 342

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 342

tccccaaagcc gttcttagacg cg 23

<210> 343

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 343

ctgggttcttc cttgcacg 18

<210> 344

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 344

gcccaaatgc cctaaggcg 28

<210> 345

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 345  
gggtgtgatg cttggaagca ttttctgtgc tttgatcact atgctaggac 50

<210> 346

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 346

gggatgcagg tggtgtctca tgggg 25

<210> 347

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 347

ccctcatgta ccggctcc 18

<210> 348

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 348

ggattctaat acgactca actatggctca gaaaagcgca acagagaa 48

<210> 349

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 349

ctatgaaatt aaccctcaact aaaggatgt cttccatgcc aaccttc 47

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&lt;212&gt; PRT

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Gln	Trp	Val	Asp	Gly	Thr	Pro	Leu	Thr	Lys	Ser	Leu	Ser	Phe	Trp
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